

Untitled
GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 974.359
Seconds

(without alignments)
944.877 Million cell

updates/sec

Title: US-10-623-880-1

Perfect score: 19

Sequence: 1 tccgttaggtgaacctgcgg 19

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | | Description |
|---------------|-------|---------|--------|------------|-------------------|
| | | Match | Length | DB ID | |
| <hr/> | | | | | |
| 1 | 19 | 100.0 | 19 | 6 AR036914 | AR036914 Sequence |
| 2 | 19 | 100.0 | 19 | 6 AR043154 | AR043154 Sequence |
| 3 | 19 | 100.0 | 19 | 6 AR050515 | AR050515 Sequence |
| 4 | 19 | 100.0 | 19 | 6 AR074654 | AR074654 Sequence |
| 5 | 19 | 100.0 | 19 | 6 AR097249 | AR097249 Sequence |
| 6 | 19 | 100.0 | 19 | 6 AR147481 | AR147481 Sequence |

| | | | | | | | Untitled | | |
|----|----|-------|-------|----|------------|----------|----------|-------------|-------------|
| 7 | 19 | 100.0 | 19 | 6 | AR153773 | | AR153773 | Sequence | |
| 8 | 19 | 100.0 | 19 | 6 | AR178320 | | AR178320 | Sequence | |
| 9 | 19 | 100.0 | 19 | 6 | BD137887 | | BD137887 | Detection | |
| 10 | 19 | 100.0 | 19 | 6 | BD188058 | | BD188058 | Method fo | |
| 11 | 19 | 100.0 | 19 | 6 | BD243828 | | BD243828 | Detection | |
| 12 | 19 | 100.0 | 19 | 6 | CQ786443 | | CQ786443 | Sequence | |
| 13 | 19 | 100.0 | 19 | 6 | CQ813043 | | CQ813043 | Sequence | |
| 14 | 19 | 100.0 | 19 | 6 | E30053 | | E30053 | Method for | |
| 15 | 19 | 100.0 | 19 | 6 | E38244 | | E38244 | Oligonucleo | |
| 16 | 19 | 100.0 | 19 | 6 | I12481 | | I12481 | Sequence 1 | |
| 17 | 19 | 100.0 | 19 | 6 | I32094 | | I32094 | Sequence 38 | |
| 18 | 19 | 100.0 | 19 | 6 | I43102 | | I43102 | Sequence 1 | |
| 19 | 19 | 100.0 | 19 | 6 | I44633 | | I44633 | Sequence 1 | |
| 20 | 19 | 100.0 | 19 | 6 | I51812 | | I51812 | Sequence 1 | |
| 21 | 19 | 100.0 | 19 | 6 | I74346 | | I74346 | Sequence 1 | |
| 22 | 19 | 100.0 | 19 | 6 | AR200612 | | AR200612 | Sequence | |
| 23 | 19 | 100.0 | 19 | 6 | AR241366 | | AR241366 | Sequence | |
| 24 | 19 | 100.0 | 19 | 6 | AR256570 | | AR256570 | Sequence | |
| 25 | 19 | 100.0 | 19 | 6 | AR429569 | | AR429569 | Sequence | |
| 26 | 19 | 100.0 | 19 | 6 | AR534210 | | AR534210 | Sequence | |
| 27 | 19 | 100.0 | 19 | 6 | AX016778 | | AX016778 | Sequence | |
| 28 | 19 | 100.0 | 19 | 6 | AX082724 | | AX082724 | Sequence | |
| 29 | 19 | 100.0 | 19 | 6 | AX195369 | | AX195369 | Sequence | |
| 30 | 19 | 100.0 | 19 | 6 | AX375721 | | AX375721 | Sequence | |
| 31 | 19 | 100.0 | 19 | 6 | AX523786 | | AX523786 | Sequence | |
| 32 | 19 | 100.0 | 19 | 6 | AX592667 | | AX592667 | Sequence | |
| 33 | 19 | 100.0 | 19 | 6 | BD003393 | | BD003393 | Methods a | |
| 34 | 19 | 100.0 | 19 | 6 | BD074168 | | BD074168 | Examinati | |
| c | 35 | 19 | 100.0 | 20 | 6 | AR159689 | | AR159689 | Sequence |
| c | 36 | 19 | 100.0 | 20 | 6 | I13120 | | I13120 | Sequence 20 |
| c | 37 | 19 | 100.0 | 20 | 6 | I33592 | | I33592 | Sequence 14 |
| c | 38 | 19 | 100.0 | 20 | 6 | BD016824 | | BD016824 | Copper-to |
| c | 39 | 19 | 100.0 | 20 | 6 | BD101856 | | BD101856 | Copper to |
| c | 40 | 19 | 100.0 | 30 | 6 | A23661 | | A23661 | Yeast 18s r |
| c | 41 | 19 | 100.0 | 30 | 6 | I20028 | | I20028 | Sequence 14 |
| 42 | 19 | 100.0 | 31 | 8 | AB032108S4 | | AB032111 | Geosmithi | |
| 43 | 19 | 100.0 | 31 | 8 | AB032112S4 | | AB032115 | Geosmithi | |
| 44 | 19 | 100.0 | 31 | 8 | AB032116S4 | | AB032119 | Geosmithi | |
| 45 | 19 | 100.0 | 31 | 8 | PC16SRR2 | | X14982 | Pneumocysti | |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 324.949
Seconds
(without alignments)
346.132 Million cell
updates/sec

Title: US-10-623-880-1
Perfect score: 19
Sequence: 1 tccgttaggtgaacctgcgg 19

Scoring table: OLIGO_NUC
Gapext 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|-------|----------------|--------|----|----------|--------------------|
| 1 | 19 | 100.0 | 19 | 2 | AAQ94390 | Aaq94390 18S ribos |
| 2 | 19 | 100.0 | 19 | 2 | AAQ91601 | Aaq91601 Candida s |
| 3 | 19 | 100.0 | 19 | 2 | AAT84759 | Aat84759 Primer IT |
| 4 | 19 | 100.0 | 19 | 2 | AAT75520 | Aat75520 Candida u |
| 5 | 19 | 100.0 | 19 | 2 | AAV62538 | Aav62538 Ribosomal |
| 6 | 19 | 100.0 | 19 | 2 | AAV59022 | Aav59022 Internal |

| | | | | | | Untitled | | |
|----|----|-------|-------|----|----------|-----------|-------------|-----------|
| 7 | 19 | 100.0 | 19 | 2 | AAV43271 | Aav43271 | PCR prime | |
| 8 | 19 | 100.0 | 19 | 2 | AAV24005 | Aav24005 | Primer IT | |
| 9 | 19 | 100.0 | 19 | 2 | AAT89973 | Aat89973 | Candida a | |
| 10 | 19 | 100.0 | 19 | 2 | AAZ09820 | Aaz09820 | Phytopht | |
| 11 | 19 | 100.0 | 19 | 2 | AAV83709 | Aav83709 | PCR prime | |
| 12 | 19 | 100.0 | 19 | 2 | AAZ06547 | Aaz06547 | Oligonucl | |
| 13 | 19 | 100.0 | 19 | 3 | AAZ60489 | Aaz60489 | PCR prime | |
| 14 | 19 | 100.0 | 19 | 3 | AAZ91727 | Aaz91727 | PCR prime | |
| 15 | 19 | 100.0 | 19 | 3 | AAZ24495 | Aazz24495 | H. capsul | |
| 16 | 19 | 100.0 | 19 | 3 | AAA92483 | Aaa92483 | Fungal ri | |
| 17 | 19 | 100.0 | 19 | 3 | AAA94771 | Aaa94771 | PCR prime | |
| 18 | 19 | 100.0 | 19 | 4 | AAF75131 | Aaf75131 | Fungal pa | |
| 19 | 19 | 100.0 | 19 | 4 | AAC93016 | Aac93016 | C. cibari | |
| 20 | 19 | 100.0 | 19 | 4 | AAS08395 | Aas08395 | Internal | |
| 21 | 19 | 100.0 | 19 | 4 | AAC91829 | Aac91829 | C. cibari | |
| 22 | 19 | 100.0 | 19 | 4 | AAC91161 | Aac91161 | Universal | |
| 23 | 19 | 100.0 | 19 | 6 | ABS70017 | Abs70017 | Aspergill | |
| 24 | 19 | 100.0 | 19 | 6 | ABA94546 | Aba94546 | Mycosphae | |
| 25 | 19 | 100.0 | 19 | 8 | ACC50003 | Acc50003 | Oligonucl | |
| 26 | 19 | 100.0 | 19 | 9 | ACC47145 | Acc47145 | Nucleotid | |
| 27 | 19 | 100.0 | 19 | 10 | ABV77013 | Abv77013 | Primer IT | |
| 28 | 19 | 100.0 | 19 | 12 | ADH61955 | Adh61955 | Panellus | |
| 29 | 19 | 100.0 | 19 | 12 | ADK23612 | Adk23612 | Fungal un | |
| 30 | 19 | 100.0 | 19 | 12 | ADM56196 | Adm56196 | Myrotheci | |
| 31 | 19 | 100.0 | 19 | 12 | ADN61575 | Adn61575 | Fungi, oo | |
| c | 32 | 19 | 100.0 | 20 | 2 | AAQ71863 | Aaq71863 | Eucaryoti |
| c | 33 | 19 | 100.0 | 20 | 2 | AAT59959 | Aat59959 | Primer TW |
| c | 34 | 19 | 100.0 | 20 | 4 | AAS08629 | Aas08629 | Cordyceps |
| c | 35 | 19 | 100.0 | 20 | 6 | AAI99898 | Aai99898 | PCR prime |
| c | 36 | 19 | 100.0 | 20 | 12 | ADH43086 | Adh43086 | NS8 prime |
| c | 37 | 19 | 100.0 | 30 | 2 | AAQ27207 | Aaq27207 | PDGF-B pr |
| c | 38 | 19 | 100.0 | 30 | 12 | ADP19598 | Adp19598 | Oligonucl |
| 39 | 19 | 100.0 | 82 | 4 | AAH26400 | Aah26400 | Arabidops | |
| 40 | 19 | 100.0 | 253 | 4 | AAH42943 | Aah42943 | Nucleic a | |
| 41 | 19 | 100.0 | 253 | 8 | ABX96743 | Abx96743 | D. melano | |
| 42 | 19 | 100.0 | 272 | 8 | ABZ55168 | Abz55168 | Aspergill | |
| 43 | 19 | 100.0 | 276 | 12 | ADL16003 | Adl16003 | White rot | |
| 44 | 19 | 100.0 | 344 | 5 | AAH42541 | Aah42541 | Nucleotid | |
| 45 | 19 | 100.0 | 345 | 4 | AAH44596 | Aah44596 | Pneumocysti | |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; search time 96.9487

Seconds

(without alignments)
320.677 Million cell

updates/sec

Title: US-10-623-880-1

Perfect score: 19

Sequence: 1 tccgttaggtgaacctgcgg 19

Scoring table: OLIGO_NUC

Gapext 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PECTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | | | | Description |
|------------|-------|---------|--------|----|------------------|--------------------|
| | | Match | Length | DB | ID | |
| 1 | 19 | 100.0 | 19 | 1 | US-08-065-845-1 | Sequence 1, Appli |
| 2 | 19 | 100.0 | 19 | 1 | US-08-233-608-38 | Sequence 38, Appli |
| 3 | 19 | 100.0 | 19 | 1 | US-08-429-523-1 | Sequence 1, Appli |
| 4 | 19 | 100.0 | 19 | 1 | US-08-429-532-1 | Sequence 1, Appli |
| 5 | 19 | 100.0 | 19 | 1 | US-08-429-522-1 | Sequence 1, Appli |
| 6 | 19 | 100.0 | 19 | 1 | US-08-429-520-1 | Sequence 1, Appli |
| 7 | 19 | 100.0 | 19 | 1 | US-08-742-023-9 | Sequence 9, Appli |
| 8 | 19 | 100.0 | 19 | 1 | US-08-887-480-38 | Sequence 38, Appli |
| 9 | 19 | 100.0 | 19 | 1 | US-08-905-314A-1 | Sequence 1, Appli |
| 10 | 19 | 100.0 | 19 | 2 | US-08-722-187-38 | Sequence 38, Appli |
| 11 | 19 | 100.0 | 19 | 3 | US-08-968-505-9 | Sequence 9, Appli |
| 12 | 19 | 100.0 | 19 | 3 | US-09-258-967-1 | Sequence 1, Appli |
| 13 | 19 | 100.0 | 19 | 3 | US-09-269-136B-1 | Sequence 1, Appli |
| 14 | 19 | 100.0 | 19 | 3 | US-09-635-747-1 | Sequence 1, Appli |

| | | | | | | Untitled | | |
|------|----|-------|-----|---|----------------------|----------|--------------------|--|
| 15 | 19 | 100.0 | 19 | 3 | US-09-026-601-1 | | Sequence 1, Appli | |
| 16 | 19 | 100.0 | 19 | 3 | US-09-673-298-1 | | Sequence 1, Appli | |
| 17 | 19 | 100.0 | 19 | 4 | US-09-481-293-1 | | Sequence 1, Appli | |
| 18 | 19 | 100.0 | 19 | 4 | US-09-939-379B-1 | | Sequence 1, Appli | |
| 19 | 19 | 100.0 | 19 | 4 | US-09-961-663-1 | | Sequence 1, Appli | |
| 20 | 19 | 100.0 | 19 | 5 | PCT-US95-04712-38 | | Sequence 38, Appli | |
| c 21 | 19 | 100.0 | 20 | 1 | US-08-093-144-20 | | Sequence 20, Appli | |
| c 22 | 19 | 100.0 | 20 | 1 | US-08-448-204-14 | | Sequence 14, Appli | |
| c 23 | 19 | 100.0 | 20 | 3 | US-09-450-656-29 | | Sequence 29, Appli | |
| c 24 | 19 | 100.0 | 30 | 1 | US-08-094-079-14 | | Sequence 14, Appli | |
| 25 | 19 | 100.0 | 261 | 4 | US-09-248-796A-13393 | | Sequence 13393, A | |
| 26 | 19 | 100.0 | 344 | 3 | US-09-488-295-1 | | Sequence 1, Appli | |
| 27 | 19 | 100.0 | 353 | 2 | US-08-722-187-84 | | Sequence 84, Appli | |
| 28 | 19 | 100.0 | 353 | 5 | PCT-US95-04712-84 | | Sequence 84, Appli | |
| 29 | 19 | 100.0 | 370 | 3 | US-09-450-656-2 | | Sequence 2, Appli | |
| 30 | 19 | 100.0 | 515 | 4 | US-09-517-790-1 | | Sequence 1, Appli | |
| 31 | 19 | 100.0 | 523 | 4 | US-09-517-790-4 | | Sequence 4, Appli | |
| 32 | 19 | 100.0 | 534 | 1 | US-08-233-608-5 | | Sequence 5, Appli | |
| 33 | 19 | 100.0 | 534 | 1 | US-08-887-480-5 | | Sequence 5, Appli | |
| 34 | 19 | 100.0 | 534 | 2 | US-08-722-187-5 | | Sequence 5, Appli | |
| 35 | 19 | 100.0 | 534 | 4 | US-09-961-663-17 | | Sequence 17, Appli | |
| 36 | 19 | 100.0 | 534 | 5 | PCT-US95-04712-5 | | Sequence 5, Appli | |
| 37 | 19 | 100.0 | 535 | 1 | US-08-742-023-1 | | Sequence 1, Appli | |
| 38 | 19 | 100.0 | 535 | 3 | US-08-968-505-1 | | Sequence 1, Appli | |
| 39 | 19 | 100.0 | 536 | 1 | US-08-742-023-2 | | Sequence 2, Appli | |
| 40 | 19 | 100.0 | 536 | 3 | US-08-968-505-2 | | Sequence 2, Appli | |
| 41 | 19 | 100.0 | 536 | 4 | US-09-517-790-5 | | Sequence 5, Appli | |
| 42 | 19 | 100.0 | 540 | 1 | US-08-233-608-6 | | Sequence 6, Appli | |
| 43 | 19 | 100.0 | 540 | 1 | US-08-887-480-6 | | Sequence 6, Appli | |
| 44 | 19 | 100.0 | 540 | 2 | US-08-722-187-6 | | Sequence 6, Appli | |
| 45 | 19 | 100.0 | 540 | 4 | US-09-961-663-18 | | Sequence 18, Appli | |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; search time 2777.9
Seconds
(without alignments)
45.570 Million cell

updates/sec

Title: US-10-623-880-1
Perfect score: 19
Sequence: 1 tccgttaggtgaacctgcgg 19

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7389322 seqs, 3331285599 residues

word size : 0

Total number of hits satisfying chosen parameters: 14778644

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:/*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:/*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:/*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:/*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:/*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:/*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:/*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:/*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:/*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:/*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:/*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:/*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:/*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:/*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:/*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:/*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:/*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:/*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:/*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:/*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:/*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:/*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:/*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:/*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:/*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Untitled
SUMMARIES

| Result No. | Score | % | Query Match | Length | DB ID | Description |
|------------|-------|-------|-------------|--------|----------------------|--------------------|
| 1 | 19 | 100.0 | 19 | 9 | US-09-961-663-1 | Sequence 1, Appli |
| 2 | 19 | 100.0 | 19 | 10 | US-09-939-379B-1 | Sequence 1, Appli |
| 3 | 19 | 100.0 | 19 | 10 | US-09-961-755A-9 | Sequence 9, Appli |
| 4 | 19 | 100.0 | 19 | 14 | US-10-199-559-1 | Sequence 1, Appli |
| 5 | 19 | 100.0 | 19 | 17 | US-10-623-880-1 | Sequence 1, Appli |
| 6 | 19 | 100.0 | 19 | 19 | US-10-468-250A-145 | Sequence 145, App |
| 7 | 19 | 100.0 | 19 | 20 | US-10-773-904-9 | Sequence 9, Appli |
| 8 | 19 | 100.0 | 19 | 20 | US-10-773-905-9 | Sequence 9, Appli |
| 9 | 19 | 100.0 | 19 | 22 | US-10-757-093-24 | Sequence 24, Appli |
| 10 | 19 | 100.0 | 19 | 22 | US-10-514-861-31 | Sequence 31, Appli |
| c 11 | 19 | 100.0 | 20 | 15 | US-10-252-093-2 | Sequence 2, Appli |
| c 12 | 19 | 100.0 | 80 | 14 | US-10-216-540-25 | Sequence 25, Appli |
| c 13 | 19 | 100.0 | 253 | 9 | US-09-768-020-59 | Sequence 59, Appli |
| c 14 | 19 | 100.0 | 345 | 18 | US-10-009-980B-7 | Sequence 7, Appli |
| c 15 | 19 | 100.0 | 359 | 19 | US-10-437-963-89865 | Sequence 89865, A |
| c 16 | 19 | 100.0 | 489 | 13 | US-10-027-632-235007 | Sequence 235007, |
| c 17 | 19 | 100.0 | 489 | 13 | US-10-027-632-235008 | Sequence 235008, |
| c 18 | 19 | 100.0 | 489 | 13 | US-10-027-632-235009 | Sequence 235009, |
| c 19 | 19 | 100.0 | 489 | 17 | US-10-027-632-235007 | Sequence 235007, |
| c 20 | 19 | 100.0 | 489 | 17 | US-10-027-632-235008 | Sequence 235008, |
| c 21 | 19 | 100.0 | 489 | 17 | US-10-027-632-235009 | Sequence 235009, |
| c 22 | 19 | 100.0 | 507 | 13 | US-10-027-632-218865 | Sequence 218865, |
| c 23 | 19 | 100.0 | 507 | 17 | US-10-027-632-218865 | Sequence 218865, |
| 24 | 19 | 100.0 | 534 | 9 | US-09-961-663-17 | Sequence 17, Appli |
| 25 | 19 | 100.0 | 540 | 9 | US-09-961-663-18 | Sequence 18, Appli |
| 26 | 19 | 100.0 | 616 | 19 | US-10-767-701-5087 | Sequence 5087, Ap |
| 27 | 19 | 100.0 | 618 | 9 | US-09-766-173C-5 | Sequence 5, Appli |
| 28 | 19 | 100.0 | 641 | 9 | US-09-766-173C-4 | Sequence 4, Appli |
| c 29 | 19 | 100.0 | 870 | 9 | US-09-897-231-4 | Sequence 4, Appli |
| c 30 | 19 | 100.0 | 874 | 9 | US-09-897-231-2 | Sequence 2, Appli |
| c 31 | 19 | 100.0 | 875 | 9 | US-09-897-231-1 | Sequence 1, Appli |
| c 32 | 19 | 100.0 | 875 | 9 | US-09-897-231-3 | Sequence 3, Appli |
| c 33 | 19 | 100.0 | 875 | 9 | US-09-897-231-5 | Sequence 5, Appli |
| c 34 | 19 | 100.0 | 875 | 9 | US-09-897-231-7 | Sequence 7, Appli |
| c 35 | 19 | 100.0 | 876 | 9 | US-09-897-231-6 | Sequence 6, Appli |
| 36 | 19 | 100.0 | 1071 | 18 | US-10-424-599-117869 | Sequence 117869, |
| 37 | 19 | 100.0 | 1193 | 9 | US-09-897-231-27 | Sequence 27, Appli |
| 38 | 19 | 100.0 | 1235 | 19 | US-10-437-963-59964 | Sequence 59964, A |
| c 39 | 19 | 100.0 | 1638 | 20 | US-10-425-115-46831 | Sequence 46831, A |
| 40 | 19 | 100.0 | 1798 | 17 | US-10-182-329-110 | Sequence 110, App |
| 41 | 19 | 100.0 | 1798 | 18 | US-10-182-327-195 | Sequence 195, App |
| 42 | 19 | 100.0 | 1798 | 19 | US-10-361-002-8 | Sequence 8, Appli |
| 43 | 19 | 100.0 | 1798 | 19 | US-10-361-004-8 | Sequence 8, Appli |
| 44 | 19 | 100.0 | 1869 | 17 | US-10-182-329-111 | Sequence 111, App |
| 45 | 19 | 100.0 | 1869 | 17 | US-10-182-329-112 | Sequence 112, App |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; search time 2543.08

Seconds

(without alignments)
284.388 Million cell

updates/sec

Title: US-10-623-880-1

Perfect score: 19

Sequence: 1 tccgttaggtgaacctgcgg 19

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | % | Description |
|------------|-------|-------------|--------|----|----|---|-------------|
| | | | | | | | |

| | | | | | | | |
|----|----|-------|-------|-----|----------|--------------------|--------------------|
| 1 | 19 | 100.0 | 50 | 1 | AU104891 | AU104891 AU104891 | |
| 2 | 19 | 100.0 | 70 | 1 | AI083317 | AI083317 SWAMCAC19 | |
| 3 | 19 | 100.0 | 72 | 7 | W91795 | W91795 SWAMCA1047S | |
| 4 | 19 | 100.0 | 73 | 2 | AW600150 | AW600150 SWL4CAK10 | |
| 5 | 19 | 100.0 | 73 | 2 | AW600166 | AW600166 SWL4CAK10 | |
| c | 19 | 100.0 | 90 | 1 | AA842703 | AA842703 MBAFCZ9E1 | |
| 6 | 19 | 100.0 | 91 | 9 | AL943905 | AL943905 Arabidops | |
| c | 7 | 19 | 100.0 | 91 | 9 | AL943905 | AL943905 Arabidops |
| 8 | 19 | 100.0 | 94 | 2 | AW140194 | AW140194 SWAMCAC44 | |
| 9 | 19 | 100.0 | 99 | 2 | AW600205 | AW600205 SWL4CAK11 | |
| 10 | 19 | 100.0 | 99 | 7 | CF356199 | CF356199 maj52e05. | |
| c | 11 | 19 | 100.0 | 106 | 2 | BE699876 | BE699876 MR0-NN008 |

| Untitled | | | | | | |
|----------|----|----|-------|-----|---|----------|
| c | 12 | 19 | 100.0 | 107 | 8 | BH428817 |
| c | 13 | 19 | 100.0 | 109 | 5 | BW443181 |
| c | 14 | 19 | 100.0 | 113 | 1 | AI066826 |
| c | 15 | 19 | 100.0 | 115 | 5 | BW442554 |
| c | 16 | 19 | 100.0 | 116 | 2 | BE758448 |
| c | 17 | 19 | 100.0 | 117 | 8 | BH526719 |
| c | 18 | 19 | 100.0 | 118 | 1 | AA232008 |
| c | 19 | 19 | 100.0 | 119 | 5 | BW227691 |
| c | 20 | 19 | 100.0 | 122 | 6 | CB884448 |
| c | 21 | 19 | 100.0 | 124 | 8 | BH443909 |
| c | 22 | 19 | 100.0 | 126 | 1 | AA661396 |
| c | 23 | 19 | 100.0 | 127 | 6 | CD374809 |
| c | 24 | 19 | 100.0 | 129 | 8 | BZ520871 |
| c | 25 | 19 | 100.0 | 130 | 8 | BZ463311 |
| c | 26 | 19 | 100.0 | 139 | 2 | BE758507 |
| c | 27 | 19 | 100.0 | 142 | 4 | BJ396485 |
| c | 28 | 19 | 100.0 | 143 | 1 | AA509105 |
| c | 29 | 19 | 100.0 | 143 | 5 | BW446696 |
| c | 30 | 19 | 100.0 | 144 | 1 | AA056801 |
| c | 31 | 19 | 100.0 | 144 | 2 | BE132429 |
| c | 32 | 19 | 100.0 | 144 | 7 | N43357 |
| c | 33 | 19 | 100.0 | 144 | 9 | AG230502 |
| c | 34 | 19 | 100.0 | 145 | 7 | CF890788 |
| c | 35 | 19 | 100.0 | 146 | 6 | CB518218 |
| c | 36 | 19 | 100.0 | 147 | 5 | BW445099 |
| c | 37 | 19 | 100.0 | 148 | 2 | AW172168 |
| c | 38 | 19 | 100.0 | 150 | 7 | CV356796 |
| c | 39 | 19 | 100.0 | 151 | 1 | AA990946 |
| c | 40 | 19 | 100.0 | 151 | 2 | BE758465 |
| c | 41 | 19 | 100.0 | 153 | 8 | CC325309 |
| c | 42 | 19 | 100.0 | 155 | 1 | AA180660 |
| c | 43 | 19 | 100.0 | 155 | 8 | CC178106 |
| c | 44 | 19 | 100.0 | 157 | 7 | CV243517 |
| c | 45 | 19 | 100.0 | 160 | 2 | AW680221 |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; search time 1025.64
Seconds

(without alignments)
944.877 Million cell

updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapext 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_p1:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | % | Description |
|---------------|-------|----------------|--------|----|----------|---|--------------------|
| | | | | | | | |
| 1 | 20 | 100.0 | 20 | 6 | AR429595 | | AR429595 Sequence |
| 2 | 20 | 100.0 | 20 | 6 | AX592693 | | AX592693 Sequence |
| c 3 | 20 | 100.0 | 460 | 8 | AF065849 | | AF065849 Venturia |
| 4 | 17 | 85.0 | 177402 | 2 | AC128077 | | AC128077 Rattus no |
| 5 | 17 | 85.0 | 236563 | 2 | AC131138 | | AC131138 Rattus no |
| c 6 | 16 | 80.0 | 458 | 8 | AF065850 | | AF065850 Cladospor |

| Untitled | | | | | | |
|----------|----|------|-----|---|----------|--------------------|
| c 7 | 16 | 80.0 | 460 | 8 | AF065848 | AF065848 Venturia |
| c 8 | 16 | 80.0 | 460 | 8 | AF065851 | AF065851 Cladospor |
| c 9 | 16 | 80.0 | 461 | 8 | AF065836 | AF065836 Venturia |
| c 10 | 16 | 80.0 | 461 | 8 | AF065837 | AF065837 Venturia |
| c 11 | 16 | 80.0 | 461 | 8 | AF065845 | AF065845 Venturia |
| c 12 | 16 | 80.0 | 461 | 8 | AF065846 | AF065846 Venturia |
| c 13 | 16 | 80.0 | 461 | 8 | AF333447 | AF333447 Venturia |
| c 14 | 16 | 80.0 | 461 | 8 | AF333448 | AF333448 Venturia |
| c 15 | 16 | 80.0 | 461 | 8 | AF333449 | AF333449 Venturia |
| c 16 | 16 | 80.0 | 461 | 8 | AF333450 | AF333450 Venturia |
| c 17 | 16 | 80.0 | 462 | 8 | AF065838 | AF065838 Venturia |
| c 18 | 16 | 80.0 | 462 | 8 | AF065839 | AF065839 Venturia |
| c 19 | 16 | 80.0 | 462 | 8 | AF065840 | AF065840 Venturia |
| c 20 | 16 | 80.0 | 462 | 8 | AF065841 | AF065841 Venturia |
| c 21 | 16 | 80.0 | 462 | 8 | AF065842 | AF065842 Venturia |
| c 22 | 16 | 80.0 | 462 | 8 | AF333440 | AF333440 Venturia |
| c 23 | 16 | 80.0 | 462 | 8 | AF333441 | AF333441 Venturia |
| c 24 | 16 | 80.0 | 462 | 8 | AF333442 | AF333442 Venturia |
| c 25 | 16 | 80.0 | 462 | 8 | AF333443 | AF333443 Venturia |
| c 26 | 16 | 80.0 | 462 | 8 | AF333444 | AF333444 Venturia |
| c 27 | 16 | 80.0 | 462 | 8 | AF333445 | AF333445 Venturia |
| c 28 | 16 | 80.0 | 462 | 8 | AF333446 | AF333446 Venturia |
| c 29 | 16 | 80.0 | 462 | 8 | AF338402 | AF338402 Spilocaea |
| c 30 | 16 | 80.0 | 463 | 8 | AF065843 | AF065843 Venturia |
| c 31 | 16 | 80.0 | 463 | 8 | AF065844 | AF065844 Venturia |
| c 32 | 16 | 80.0 | 463 | 8 | AF065847 | AF065847 Venturia |
| c 33 | 16 | 80.0 | 463 | 8 | AF338399 | AF338399 Spilocaea |
| c 34 | 16 | 80.0 | 463 | 8 | AF338400 | AF338400 Spilocaea |
| c 35 | 16 | 80.0 | 463 | 8 | AF338401 | AF338401 Spilocaea |
| c 36 | 16 | 80.0 | 491 | 8 | AY251085 | AY251085 Fusicladi |
| c 37 | 16 | 80.0 | 492 | 8 | AY251084 | AY251084 Fusicladi |
| c 38 | 16 | 80.0 | 501 | 8 | AY173018 | AY173018 Venturia |
| c 39 | 16 | 80.0 | 501 | 8 | AY177406 | AY177406 Venturia |
| c 40 | 16 | 80.0 | 515 | 8 | AY251082 | AY251082 Fusicladi |
| c 41 | 16 | 80.0 | 518 | 8 | AY251083 | AY251083 Pseudocla |
| c 42 | 16 | 80.0 | 522 | 8 | AF531078 | AF531078 Venturia |
| c 43 | 16 | 80.0 | 532 | 8 | AF333438 | AF333438 Venturia |
| c 44 | 16 | 80.0 | 541 | 8 | AY361999 | AY361999 Fusicladi |
| c 45 | 16 | 80.0 | 541 | 8 | AF393685 | AF393685 Fusicladi |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 342.051
Seconds

(without alignments)
346.132 Million cell

updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapext 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | % | Description |
|---------------|-------|----------------|--------|----|----------|---|--------------------|
| | | | | | | | |
| c 1 | 20 | 100.0 | 20 | 10 | ABV77037 | | Abv77037 Primer vc |
| c 2 | 16 | 80.0 | 600 | 10 | ADG37681 | | Adg37681 Aspergill |
| c 3 | 16 | 80.0 | 1662 | 5 | AAH65558 | | Aah65558 C glutami |
| 4 | 16 | 80.0 | 3602 | 10 | ADB69027 | | Adb69027 C. neofor |
| 5 | 16 | 80.0 | 349980 | 5 | AAH68525 | | Aah68525 C glutami |
| 6 | 15 | 75.0 | 510 | 6 | ABQ26634 | | Abq26634 oligonucl |
| c 7 | 15 | 75.0 | 510 | 6 | ABQ26635 | | Abq26635 oligonucl |

| Untitled | | | | | | | | |
|----------|----|----|------|--------|----|-------------|--------------|-----------|
| c | 8 | 15 | 75.0 | 1176 | 8 | ACA32188 | Aca32188 | Prokaryot |
| c | 9 | 15 | 75.0 | 1400 | 3 | AAZ49433 | Aaz49433 | E.coli K |
| c | 10 | 15 | 75.0 | 1468 | 6 | ABQ48562 | Abq48562 | Oligonucl |
| c | 11 | 15 | 75.0 | 1468 | 6 | ABQ48563 | Abq48563 | Oligonucl |
| c | 12 | 15 | 75.0 | 22130 | 6 | ABS78850 | Abs78850 | E. coli C |
| c | 13 | 15 | 75.0 | 22130 | 10 | ADH80417 | Adh80417 | Escherich |
| c | 14 | 15 | 75.0 | 26173 | 9 | ACD19056 | Acd19056 | E. coli O |
| c | 15 | 15 | 75.0 | 38155 | 9 | ACD19066 | Acd19066 | E. coli O |
| c | 16 | 15 | 75.0 | 44029 | 10 | ADC00710 | Adc00710 | Enterohae |
| c | 17 | 15 | 75.0 | 45175 | 9 | ACD19103 | Acd19103 | E.coli O |
| c | 18 | 15 | 75.0 | 48423 | 10 | ADC00439 | Adc00439 | Enterohae |
| c | 19 | 15 | 75.0 | 49650 | 10 | ADC00365 | Adc00365 | Enterohae |
| c | 20 | 15 | 75.0 | 49795 | 9 | ACD19047 | Acd19047 | E.coli O |
| c | 21 | 15 | 75.0 | 58175 | 10 | ADC00292 | Adc00292 | Enterohae |
| c | 22 | 15 | 75.0 | 91740 | 10 | ADC00956 | Adc00956 | Enterohae |
| c | 23 | 15 | 75.0 | 110000 | 12 | ADN46845_01 | Continuation | (2 of |
| c | 24 | 15 | 75.0 | 110000 | 12 | ADN47591_18 | Continuation | (19 o |
| c | 25 | 15 | 75.0 | 110000 | 12 | ADN47591_19 | Continuation | (20 o |
| c | 26 | 15 | 75.0 | 110000 | 12 | ADN46123_01 | Continuation | (2 of |
| c | 27 | 15 | 75.0 | 110000 | 12 | ADN47209_18 | Continuation | (19 o |
| c | 28 | 15 | 75.0 | 110000 | 12 | ADN47209_19 | Continuation | (20 o |
| c | 29 | 15 | 75.0 | 110000 | 12 | ADN46464_01 | Continuation | (2 of |
| c | 30 | 15 | 75.0 | 110000 | 12 | ADN47960_18 | Continuation | (19 o |
| c | 31 | 15 | 75.0 | 110000 | 12 | ADN47960_19 | Continuation | (20 o |
| c | 32 | 15 | 75.0 | 134141 | 6 | ABN83487 | Abn83487 | Escherich |
| c | 33 | 14 | 70.0 | 232 | 4 | AAF79990 | Aaf79990 | Nucleotid |
| c | 34 | 14 | 70.0 | 289 | 2 | AAV88814 | Aav88814 | EST clone |
| c | 35 | 14 | 70.0 | 300 | 2 | AAZ14988 | Aaz14988 | Human gen |
| c | 36 | 14 | 70.0 | 303 | 5 | AAS86933 | Aas86933 | DNA encod |
| c | 37 | 14 | 70.0 | 405 | 4 | AAF83395 | Aaf83395 | P. chryso |
| c | 38 | 14 | 70.0 | 405 | 4 | AAF83396 | Aaf83396 | P. chryso |
| c | 39 | 14 | 70.0 | 451 | 9 | ACH27903 | Ach27903 | Human adu |
| c | 40 | 14 | 70.0 | 558 | 13 | ADQ78945 | Adq78945 | Novel can |
| c | 41 | 14 | 70.0 | 643 | 8 | ABX63812 | Abx63812 | Human cDN |
| c | 42 | 14 | 70.0 | 649 | 13 | ACN54120 | Acn54120 | Cotton an |
| c | 43 | 14 | 70.0 | 726 | 8 | ACF39401 | Acf39401 | Mycobacte |
| c | 44 | 14 | 70.0 | 831 | 4 | AAH06449 | Aah06449 | Human cDN |
| c | 45 | 14 | 70.0 | 834 | 11 | ACN92285 | Acn92285 | Breast ca |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; search time 102.051
Seconds
(without alignments)
320.677 Million cell
updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 cccggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:/*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:/*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:/*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:/*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:/*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

| Result No. | Score | SUMMARIES | | | | | Description |
|---------------|-------|-----------|-------|--------|---------------------|----|-------------------|
| | | Query | Match | Length | DB | ID | |
| 1 | 20 | 100.0 | 20 | 4 | US-09-939-379B-27 | | Sequence 27, Appl |
| c 2 | 15 | 75.0 | 26173 | 3 | US-09-453-702B-69 | | Sequence 69, Appl |
| c 3 | 15 | 75.0 | 38155 | 3 | US-09-453-702B-79 | | Sequence 79, Appl |
| c 4 | 15 | 75.0 | 45175 | 3 | US-09-453-702B-116 | | Sequence 116, App |
| c 5 | 15 | 75.0 | 49795 | 3 | US-09-453-702B-60 | | Sequence 60, Appl |
| c 6 | 14 | 70.0 | 1281 | 4 | US-09-902-540-7744 | | Sequence 7744, Ap |
| c 7 | 14 | 70.0 | 1309 | 2 | US-08-933-750C-63 | | Sequence 63, Appl |
| c 8 | 14 | 70.0 | 1309 | 3 | US-09-234-613-63 | | Sequence 63, Appl |
| c 9 | 14 | 70.0 | 2513 | 4 | US-09-016-434-1166 | | Sequence 1166, Ap |
| c 10 | 14 | 70.0 | 2513 | 4 | US-09-949-016-904 | | Sequence 904, App |
| c 11 | 14 | 70.0 | 2521 | 4 | US-09-949-016-1755 | | Sequence 1755, Ap |
| c 12 | 14 | 70.0 | 5641 | 4 | US-09-902-540-767 | | Sequence 767, App |
| c 13 | 14 | 70.0 | 12453 | 4 | US-09-949-016-12646 | | Sequence 12646, A |
| c 14 | 14 | 70.0 | 12460 | 4 | US-09-949-016-13497 | | Sequence 13497, A |

| Untitled | | | | | | | |
|----------|----|----|------|---------|---|----------------------|--------------------|
| | 15 | 14 | 70.0 | 16442 | 3 | US-08-781-891-208 | Sequence 208, App |
| c | 16 | 14 | 70.0 | 16442 | 4 | US-09-618-166-208 | Sequence 208, App |
| | 17 | 14 | 70.0 | 28136 | 4 | US-09-949-016-16317 | Sequence 16317, A |
| | 18 | 14 | 70.0 | 52971 | 4 | US-09-949-016-16452 | Sequence 16452, A |
| | 19 | 14 | 70.0 | 89716 | 4 | US-09-949-016-11900 | Sequence 11900, A |
| c | 20 | 14 | 70.0 | 670689 | 4 | US-09-949-016-12505 | Sequence 12505, A |
| c | 21 | 14 | 70.0 | 670690 | 4 | US-09-949-016-14207 | Sequence 14207, A |
| c | 22 | 14 | 70.0 | 784019 | 4 | US-09-949-016-14033 | Sequence 14033, A |
| c | 23 | 14 | 70.0 | 828152 | 4 | US-09-949-016-12777 | Sequence 12777, A |
| | 24 | 14 | 70.0 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appli |
| | 25 | 14 | 70.0 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli |
| | 26 | 13 | 65.0 | 16 | 4 | US-09-939-379B-25 | Sequence 25, Appli |
| c | 27 | 13 | 65.0 | 219 | 3 | US-09-056-556-218 | Sequence 218, App |
| c | 28 | 13 | 65.0 | 219 | 3 | US-09-072-596-213 | Sequence 213, App |
| c | 29 | 13 | 65.0 | 219 | 4 | US-09-072-967-218 | Sequence 218, App |
| | 30 | 13 | 65.0 | 243 | 4 | US-09-252-991A-4273 | Sequence 4273, Ap |
| | 31 | 13 | 65.0 | 352 | 2 | US-08-692-511-1 | Sequence 1, Appli |
| c | 32 | 13 | 65.0 | 355 | 3 | US-09-328-111-558 | Sequence 558, App |
| c | 33 | 13 | 65.0 | 522 | 1 | US-07-778-156-4 | Sequence 4, Appli |
| c | 34 | 13 | 65.0 | 522 | 2 | US-08-422-166-4 | Sequence 4, Appli |
| c | 35 | 13 | 65.0 | 563 | 3 | US-09-385-982-434 | Sequence 434, App |
| | 36 | 13 | 65.0 | 601 | 4 | US-09-949-016-79117 | Sequence 79117, A |
| | 37 | 13 | 65.0 | 601 | 4 | US-09-949-016-79118 | Sequence 79118, A |
| | 38 | 13 | 65.0 | 601 | 4 | US-09-949-016-79119 | Sequence 79119, A |
| | 39 | 13 | 65.0 | 601 | 4 | US-09-949-016-79120 | Sequence 79120, A |
| c | 40 | 13 | 65.0 | 601 | 4 | US-09-949-016-83352 | Sequence 83352, A |
| c | 41 | 13 | 65.0 | 601 | 4 | US-09-949-016-107767 | Sequence 107767, |
| c | 42 | 13 | 65.0 | 601 | 4 | US-09-949-016-107768 | Sequence 107768, |
| c | 43 | 13 | 65.0 | 601 | 4 | US-09-949-016-165565 | Sequence 165565, |
| c | 44 | 13 | 65.0 | 601 | 4 | US-09-949-016-206916 | Sequence 206916, |
| | 45 | 13 | 65.0 | 610 | 3 | US-09-385-982-229 | Sequence 229, App |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 2924.1
Seconds
(without alignments)
45.570 Million cell

updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7389322 seqs, 3331285599 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14778644

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:/*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:/*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:/*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:/*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:/*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:/*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:/*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:/*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:/*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:/*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:/*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:/*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:/*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:/*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:/*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:/*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:/*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:/*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:/*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:/*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:/*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:/*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:/*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:/*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:/*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Untitled
SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------------------------|-------------------|
| c 1 | 20 | 100.0 | 20 | 10 US-09-939-379B-27 | Sequence 27, Appl |
| c 2 | 20 | 100.0 | 20 | 14 US-10-199-559-27 | Sequence 27, Appl |
| c 3 | 20 | 100.0 | 20 | 17 US-10-623-880-27 | Sequence 27, Appl |
| c 4 | 16 | 80.0 | 1662 | 9 US-09-738-626-593 | Sequence 593, App |
| c 5 | 16 | 80.0 | 3602 | 17 US-10-320-797-154 | Sequence 154, App |
| c 6 | 16 | 80.0 | 3309400 | 9 US-09-738-626-1 | Sequence 1, Appli |
| c 7 | 15 | 75.0 | 136 | 19 US-10-437-963-38131 | Sequence 38131, A |
| c 8 | 15 | 75.0 | 453 | 15 US-10-156-761-1914 | Sequence 1914, Ap |
| c 9 | 15 | 75.0 | 510 | 20 US-10-363-345A-13225 | Sequence 13225, A |
| c 10 | 15 | 75.0 | 510 | 20 US-10-363-345A-13226 | Sequence 13226, A |
| c 11 | 15 | 75.0 | 510 | 21 US-10-363-483A-13225 | Sequence 13225, A |
| c 12 | 15 | 75.0 | 510 | 21 US-10-363-483A-13226 | Sequence 13226, A |
| c 13 | 15 | 75.0 | 619 | 20 US-10-425-115-134035 | Sequence 134035, |
| c 14 | 15 | 75.0 | 1176 | 17 US-10-282-122A-20058 | Sequence 20058, A |
| c 15 | 15 | 75.0 | 1292 | 18 US-10-425-114-18323 | Sequence 18323, A |
| c 16 | 15 | 75.0 | 1389 | 20 US-10-425-115-149422 | Sequence 149422, |
| c 17 | 15 | 75.0 | 1468 | 20 US-10-363-345A-35153 | Sequence 35153, A |
| c 18 | 15 | 75.0 | 1468 | 20 US-10-363-345A-35154 | Sequence 35154, A |
| c 19 | 15 | 75.0 | 1468 | 21 US-10-363-483A-35153 | Sequence 35153, A |
| c 20 | 15 | 75.0 | 1468 | 21 US-10-363-483A-35154 | Sequence 35154, A |
| c 21 | 15 | 75.0 | 22130 | 16 US-10-085-959-17 | Sequence 17, Appl |
| c 22 | 15 | 75.0 | 26173 | 14 US-10-114-170-69 | Sequence 69, Appl |
| c 23 | 15 | 75.0 | 38155 | 14 US-10-114-170-79 | Sequence 79, Appl |
| c 24 | 15 | 75.0 | 45175 | 14 US-10-114-170-116 | Sequence 116, App |
| c 25 | 15 | 75.0 | 49795 | 14 US-10-114-170-60 | Sequence 60, Appl |
| c 26 | 15 | 75.0 | 72480 | 17 US-10-418-837-2 | Sequence 2, Appli |
| c 27 | 15 | 75.0 | 9025608 | 15 US-10-156-761-1 | Sequence 1, Appli |
| c 28 | 14 | 70.0 | 25 | 21 US-10-719-900-467742 | Sequence 467742, |
| c 29 | 14 | 70.0 | 25 | 21 US-10-719-900-972064 | Sequence 972064, |
| c 30 | 14 | 70.0 | 25 | 22 US-10-719-956-214222 | Sequence 214222, |
| c 31 | 14 | 70.0 | 25 | 22 US-10-719-956-692586 | Sequence 692586, |
| c 32 | 14 | 70.0 | 232 | 14 US-10-070-676-24 | Sequence 24, Appl |
| c 33 | 14 | 70.0 | 289 | 13 US-10-040-739-1292 | Sequence 1292, Ap |
| c 34 | 14 | 70.0 | 303 | 22 US-10-450-763-22737 | Sequence 22737, A |
| c 35 | 14 | 70.0 | 451 | 10 US-09-918-995-15115 | Sequence 15115, A |
| c 36 | 14 | 70.0 | 471 | 20 US-10-425-115-92035 | Sequence 92035, A |
| c 37 | 14 | 70.0 | 600 | 22 US-10-972-079-86660 | Sequence 86660, A |
| c 38 | 14 | 70.0 | 643 | 13 US-10-044-090-812 | Sequence 812, App |
| c 39 | 14 | 70.0 | 649 | 19 US-10-021-323-8901 | Sequence 8901, Ap |
| c 40 | 14 | 70.0 | 810 | 13 US-10-027-632-7665 | Sequence 7665, Ap |
| c 41 | 14 | 70.0 | 810 | 17 US-10-027-632-7665 | Sequence 7665, Ap |
| c 42 | 14 | 70.0 | 811 | 13 US-10-027-632-166429 | Sequence 166429, |
| c 43 | 14 | 70.0 | 811 | 13 US-10-027-632-166430 | Sequence 166430, |
| c 44 | 14 | 70.0 | 811 | 13 US-10-027-632-166431 | Sequence 166431, |
| c 45 | 14 | 70.0 | 811 | 13 US-10-027-632-166432 | Sequence 166432, |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 2924.1
Seconds
(without alignments)

45.570 Million cell

updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapext 60.0 , Gapext 60.0

Searched: 7389322 seqs, 3331285599 residues

word size : 0

Total number of hits satisfying chosen parameters: 14778644

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:/*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:/*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:/*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:/*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:/*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:/*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:/*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:/*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:/*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:/*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:/*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:/*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:/*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:/*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:/*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:/*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:/*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:/*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:/*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:/*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:/*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:/*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:/*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:/*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:/*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Untitled
SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------------------------|-------------------|
| c 1 | 20 | 100.0 | 20 | 10 US-09-939-379B-27 | Sequence 27, Appl |
| c 2 | 20 | 100.0 | 20 | 14 US-10-199-559-27 | Sequence 27, Appl |
| c 3 | 20 | 100.0 | 20 | 17 US-10-623-880-27 | Sequence 27, Appl |
| c 4 | 16 | 80.0 | 1662 | 9 US-09-738-626-593 | Sequence 593, App |
| c 5 | 16 | 80.0 | 3602 | 17 US-10-320-797-154 | Sequence 154, App |
| c 6 | 16 | 80.0 | 3309400 | 9 US-09-738-626-1 | Sequence 1, Appli |
| c 7 | 15 | 75.0 | 136 | 19 US-10-437-963-38131 | Sequence 38131, A |
| c 8 | 15 | 75.0 | 453 | 15 US-10-156-761-1914 | Sequence 1914, Ap |
| c 9 | 15 | 75.0 | 510 | 20 US-10-363-345A-13225 | Sequence 13225, A |
| c 10 | 15 | 75.0 | 510 | 20 US-10-363-345A-13226 | Sequence 13226, A |
| c 11 | 15 | 75.0 | 510 | 21 US-10-363-483A-13225 | Sequence 13225, A |
| c 12 | 15 | 75.0 | 510 | 21 US-10-363-483A-13226 | Sequence 13226, A |
| c 13 | 15 | 75.0 | 619 | 20 US-10-425-115-134035 | Sequence 134035, |
| c 14 | 15 | 75.0 | 1176 | 17 US-10-282-122A-20058 | Sequence 20058, A |
| c 15 | 15 | 75.0 | 1292 | 18 US-10-425-114-18323 | Sequence 18323, A |
| c 16 | 15 | 75.0 | 1389 | 20 US-10-425-115-149422 | Sequence 149422, |
| c 17 | 15 | 75.0 | 1468 | 20 US-10-363-345A-35153 | Sequence 35153, A |
| c 18 | 15 | 75.0 | 1468 | 20 US-10-363-345A-35154 | Sequence 35154, A |
| c 19 | 15 | 75.0 | 1468 | 21 US-10-363-483A-35153 | Sequence 35153, A |
| c 20 | 15 | 75.0 | 1468 | 21 US-10-363-483A-35154 | Sequence 35154, A |
| c 21 | 15 | 75.0 | 22130 | 16 US-10-085-959-17 | Sequence 17, Appl |
| c 22 | 15 | 75.0 | 26173 | 14 US-10-114-170-69 | Sequence 69, Appl |
| c 23 | 15 | 75.0 | 38155 | 14 US-10-114-170-79 | Sequence 79, Appl |
| c 24 | 15 | 75.0 | 45175 | 14 US-10-114-170-116 | Sequence 116, App |
| c 25 | 15 | 75.0 | 49795 | 14 US-10-114-170-60 | Sequence 60, Appl |
| c 26 | 15 | 75.0 | 72480 | 17 US-10-418-837-2 | Sequence 2, Appli |
| c 27 | 15 | 75.0 | 9025608 | 15 US-10-156-761-1 | Sequence 1, Appli |
| c 28 | 14 | 70.0 | 25 | 21 US-10-719-900-467742 | Sequence 467742, |
| c 29 | 14 | 70.0 | 25 | 21 US-10-719-900-972064 | Sequence 972064, |
| c 30 | 14 | 70.0 | 25 | 22 US-10-719-956-214222 | Sequence 214222, |
| c 31 | 14 | 70.0 | 25 | 22 US-10-719-956-692586 | Sequence 692586, |
| c 32 | 14 | 70.0 | 232 | 14 US-10-070-676-24 | Sequence 24, Appl |
| c 33 | 14 | 70.0 | 289 | 13 US-10-040-739-1292 | Sequence 1292, Ap |
| c 34 | 14 | 70.0 | 303 | 22 US-10-450-763-22737 | Sequence 22737, A |
| c 35 | 14 | 70.0 | 451 | 10 US-09-918-995-15115 | Sequence 15115, A |
| c 36 | 14 | 70.0 | 471 | 20 US-10-425-115-92035 | Sequence 92035, A |
| c 37 | 14 | 70.0 | 600 | 22 US-10-972-079-86660 | Sequence 86660, A |
| c 38 | 14 | 70.0 | 643 | 13 US-10-044-090-812 | Sequence 812, App |
| c 39 | 14 | 70.0 | 649 | 19 US-10-021-323-8901 | Sequence 8901, Ap |
| c 40 | 14 | 70.0 | 810 | 13 US-10-027-632-7665 | Sequence 7665, Ap |
| c 41 | 14 | 70.0 | 810 | 17 US-10-027-632-7665 | Sequence 7665, Ap |
| c 42 | 14 | 70.0 | 811 | 13 US-10-027-632-166429 | Sequence 166429, |
| c 43 | 14 | 70.0 | 811 | 13 US-10-027-632-166430 | Sequence 166430, |
| c 44 | 14 | 70.0 | 811 | 13 US-10-027-632-166431 | Sequence 166431, |
| c 45 | 14 | 70.0 | 811 | 13 US-10-027-632-166432 | Sequence 166432, |

Untitled

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 10:52:09 ; Search time 2676.92
Seconds
(without alignments)
284.388 Million cell
updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapext 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|-------|----------------|--------|----|----------|--------------------|
| 1 | 17 | 85.0 | 431 | 6 | CD785534 | CD785534 EST656895 |
| 2 | 17 | 85.0 | 466 | 2 | BF856215 | BF856215 CM4-FN019 |
| 3 | 17 | 85.0 | 792 | 6 | CD786033 | CD786033 EST657394 |
| 4 | 17 | 85.0 | 893 | 6 | CD794511 | CD794511 EST665872 |
| c 5 | 16 | 80.0 | 467 | 7 | CK179037 | CK179037 EST768357 |
| c 6 | 16 | 80.0 | 479 | 9 | CG679733 | CG679733 ZMMBBb031 |
| 7 | 16 | 80.0 | 521 | 7 | CK437458 | CK437458 GQ0041.BR |
| 8 | 16 | 80.0 | 527 | 7 | CO473798 | CO473798 GQ0045.B3 |
| 9 | 16 | 80.0 | 532 | 8 | AZ069108 | AZ069108 RPCI-23-4 |
| c 10 | 16 | 80.0 | 544 | 5 | BU362724 | BU362724 603787416 |

Untitled

| | | | | | | | |
|---|----|----|------|------|---|----------|--------------------|
| c | 11 | 16 | 80.0 | 546 | 7 | CO474354 | CO474354 GQ0045.B3 |
| c | 12 | 16 | 80.0 | 556 | 9 | CG913575 | CG913575 ZMMBBb037 |
| | 13 | 16 | 80.0 | 573 | 7 | CK179036 | CK179036 EST768356 |
| | 14 | 16 | 80.0 | 710 | 9 | AG300383 | AG300383 Mus muscu |
| | 15 | 16 | 80.0 | 711 | 4 | BG569377 | BG569377 602588695 |
| | 16 | 16 | 80.0 | 724 | 5 | BU000509 | BU000509 QGG25A09. |
| c | 17 | 16 | 80.0 | 752 | 9 | CG795593 | CG795593 ZMMBBb032 |
| | 18 | 16 | 80.0 | 791 | 9 | CG689000 | CG689000 ZMMBBC012 |
| | 19 | 16 | 80.0 | 827 | 9 | CG180063 | CG180063 PUIFS71TD |
| c | 20 | 16 | 80.0 | 862 | 9 | CNS03ARJ | AL235576 Tetraodon |
| c | 21 | 16 | 80.0 | 867 | 7 | CN833033 | CN833033 AGENCOURT |
| | 22 | 16 | 80.0 | 928 | 9 | CG077859 | CG077859 PUJDF38TB |
| c | 23 | 16 | 80.0 | 948 | 8 | BZ081313 | BZ081313 lkf87d06. |
| | 24 | 16 | 80.0 | 1003 | 9 | CL199390 | CL199390 ZMMBBC007 |
| c | 25 | 16 | 80.0 | 1153 | 9 | AG128376 | AG128376 Pan trogl |
| c | 26 | 15 | 75.0 | 112 | 4 | BM516383 | BM516383 kj69e02.y |
| c | 27 | 15 | 75.0 | 273 | 7 | CF327617 | CF327617 NACL--02- |
| | 28 | 15 | 75.0 | 305 | 8 | AZ577615 | AZ577615 11h09 Sho |
| | 29 | 15 | 75.0 | 340 | 1 | AA807740 | AA807740 nw27c12.s |
| c | 30 | 15 | 75.0 | 420 | 1 | AJ480572 | AJ480572 AJ480572 |
| c | 31 | 15 | 75.0 | 439 | 9 | CG998755 | CG998755 ZMMBBb053 |
| c | 32 | 15 | 75.0 | 454 | 2 | BE367271 | BE367271 PI1_44_E0 |
| c | 33 | 15 | 75.0 | 458 | 4 | BG355454 | BG355454 EM1_16_F0 |
| | 34 | 15 | 75.0 | 466 | 2 | AW340130 | AW340130 hc93f12.x |
| c | 35 | 15 | 75.0 | 477 | 4 | BM319936 | BM319936 ki80f05.y |
| | 36 | 15 | 75.0 | 477 | 7 | CK149415 | CK149415 17420TEX5 |
| c | 37 | 15 | 75.0 | 485 | 5 | BU979426 | BU979426 HA16C02r |
| c | 38 | 15 | 75.0 | 491 | 4 | BG280699 | BG280699 c5g08np.r |
| c | 39 | 15 | 75.0 | 499 | 2 | BE455006 | BE455006 HVSMEh009 |
| c | 40 | 15 | 75.0 | 499 | 4 | BM374819 | BM374819 EBma05_SQ |
| c | 41 | 15 | 75.0 | 533 | 7 | CK149461 | CK149461 17420TEX6 |
| c | 42 | 15 | 75.0 | 552 | 5 | BU979447 | BU979447 HA16D03r |
| | 43 | 15 | 75.0 | 600 | 7 | CF753483 | CF753483 EST-Conti |
| c | 44 | 15 | 75.0 | 607 | 5 | BU983985 | BU983985 HA31k06r |
| | 45 | 15 | 75.0 | 613 | 9 | CL912826 | CL912826 OA_ABa001 |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 13:04:33 ; Search time 1819 Seconds
(without alignments)
506.129 Million cell

updates/sec

Title: US-10-623-880-1

Perfect score: 19

Sequence: 1 tccgttagtgaacctgcgg 19

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 578008

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description | |
|---------------|-------|----------------|--------|----|----------|-------------|----------|
| | | | | | | % | |
| 1 | 19 | 100.0 | 19 | 6 | AR036914 | AR036914 | Sequence |
| 2 | 19 | 100.0 | 19 | 6 | AR043154 | AR043154 | Sequence |
| 3 | 19 | 100.0 | 19 | 6 | AR050515 | AR050515 | Sequence |
| 4 | 19 | 100.0 | 19 | 6 | AR074654 | AR074654 | Sequence |
| 5 | 19 | 100.0 | 19 | 6 | AR097249 | AR097249 | Sequence |
| 6 | 19 | 100.0 | 19 | 6 | AR147481 | AR147481 | Sequence |
| 7 | 19 | 100.0 | 19 | 6 | AR153773 | AR153773 | Sequence |

Untitled

| | | | | | | | |
|----|----|-------|------|----|----------|--------------------|-------------------|
| 8 | 19 | 100.0 | 19 | 6 | AR178320 | AR178320 Sequence | |
| 9 | 19 | 100.0 | 19 | 6 | BD137887 | BD137887 Detection | |
| 10 | 19 | 100.0 | 19 | 6 | BD188058 | BD188058 Method fo | |
| 11 | 19 | 100.0 | 19 | 6 | BD243828 | BD243828 Detection | |
| 12 | 19 | 100.0 | 19 | 6 | CQ786443 | CQ786443 Sequence | |
| 13 | 19 | 100.0 | 19 | 6 | CQ813043 | CQ813043 Sequence | |
| 14 | 19 | 100.0 | 19 | 6 | E30053 | E30053 Method for | |
| 15 | 19 | 100.0 | 19 | 6 | E38244 | E38244 Oligonucleo | |
| 16 | 19 | 100.0 | 19 | 6 | I12481 | I12481 Sequence 1 | |
| 17 | 19 | 100.0 | 19 | 6 | I32094 | I32094 Sequence 38 | |
| 18 | 19 | 100.0 | 19 | 6 | I43102 | I43102 Sequence 1 | |
| 19 | 19 | 100.0 | 19 | 6 | I44633 | I44633 Sequence 1 | |
| 20 | 19 | 100.0 | 19 | 6 | I51812 | I51812 Sequence 1 | |
| 21 | 19 | 100.0 | 19 | 6 | I74346 | I74346 Sequence 1 | |
| 22 | 19 | 100.0 | 19 | 6 | AR200612 | AR200612 Sequence | |
| 23 | 19 | 100.0 | 19 | 6 | AR241366 | AR241366 Sequence | |
| 24 | 19 | 100.0 | 19 | 6 | AR256570 | AR256570 Sequence | |
| 25 | 19 | 100.0 | 19 | 6 | AR429569 | AR429569 Sequence | |
| 26 | 19 | 100.0 | 19 | 6 | AR534210 | AR534210 Sequence | |
| 27 | 19 | 100.0 | 19 | 6 | AX016778 | AX016778 Sequence | |
| 28 | 19 | 100.0 | 19 | 6 | AX082724 | AX082724 Sequence | |
| 29 | 19 | 100.0 | 19 | 6 | AX195369 | AX195369 Sequence | |
| 30 | 19 | 100.0 | 19 | 6 | AX375721 | AX375721 Sequence | |
| 31 | 19 | 100.0 | 19 | 6 | AX523786 | AX523786 Sequence | |
| 32 | 19 | 100.0 | 19 | 6 | AX592667 | AX592667 Sequence | |
| 33 | 19 | 100.0 | 19 | 6 | BD003393 | BD003393 Methods a | |
| 34 | 19 | 100.0 | 19 | 6 | BD074168 | BD074168 Examinati | |
| c | 35 | 17 | 89.5 | 19 | 6 | CQ868753 | CQ868753 Sequence |
| c | 36 | 16 | 84.2 | 17 | 6 | AR186637 | AR186637 Sequence |
| c | 37 | 16 | 84.2 | 17 | 6 | AR186638 | AR186638 Sequence |
| c | 38 | 16 | 84.2 | 17 | 6 | AR323268 | AR323268 Sequence |
| c | 39 | 16 | 84.2 | 17 | 6 | AR323269 | AR323269 Sequence |
| c | 40 | 16 | 84.2 | 19 | 6 | CQ830761 | CQ830761 Sequence |
| c | 41 | 15 | 78.9 | 17 | 6 | AR327596 | AR327596 Sequence |
| 42 | 15 | 78.9 | 18 | 6 | CQ848503 | CQ848503 Sequence | |
| 43 | 13 | 68.4 | 13 | 6 | AR082394 | AR082394 Sequence | |
| c | 44 | 13 | 68.4 | 17 | 6 | AR327597 | AR327597 Sequence |
| c | 45 | 12 | 63.2 | 17 | 6 | AR327595 | AR327595 Sequence |

Untitled
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 12:19:43 ; Search time 417 Seconds
(without alignments)
269.724 Million cell

updates/sec

Title: US-10-623-880-1

Perfect score: 19

Sequence: 1 tccgttaggtgaacctgcgg 19

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1679476

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | % | Description |
|---------------|-------|----------------|--------|----|----------|----------|-------------|
| | | | | | | | |
| 1 | 19 | 100.0 | 19 | 2 | AAQ94390 | Aaq94390 | 18S ribos |
| 2 | 19 | 100.0 | 19 | 2 | AAQ91601 | Aaq91601 | Candida s |
| 3 | 19 | 100.0 | 19 | 2 | AAT84759 | Aat84759 | Primer IT |
| 4 | 19 | 100.0 | 19 | 2 | AAT75520 | Aat75520 | Candida u |
| 5 | 19 | 100.0 | 19 | 2 | AAV62538 | Aav62538 | Ribosomal |
| 6 | 19 | 100.0 | 19 | 2 | AAV59022 | Aav59022 | Internal |
| 7 | 19 | 100.0 | 19 | 2 | AAV43271 | Aav43271 | PCR prime |
| 8 | 19 | 100.0 | 19 | 2 | AAV24005 | Aav24005 | Primer IT |

| Untitled | | | | | | | |
|----------|----|-------|------|----|----------|--------------------|--------------------|
| 9 | 19 | 100.0 | 19 | 2 | AAT89973 | Aat89973 Candida a | |
| 10 | 19 | 100.0 | 19 | 2 | AAZ09820 | Aaz09820 Phytophth | |
| 11 | 19 | 100.0 | 19 | 2 | AAV83709 | Aav83709 PCR prime | |
| 12 | 19 | 100.0 | 19 | 2 | AAZ06547 | Aaz06547 Oligonucl | |
| 13 | 19 | 100.0 | 19 | 3 | AAZ60489 | Aaz60489 PCR prime | |
| 14 | 19 | 100.0 | 19 | 3 | AAZ91727 | Aaz91727 PCR prime | |
| 15 | 19 | 100.0 | 19 | 3 | AAZ24495 | Aaz24495 H. capsul | |
| 16 | 19 | 100.0 | 19 | 3 | AAA92483 | Aaa92483 Fungal ri | |
| 17 | 19 | 100.0 | 19 | 3 | AAA94771 | Aaa94771 PCR prime | |
| 18 | 19 | 100.0 | 19 | 4 | AAF75131 | Aaf75131 Fungal pa | |
| 19 | 19 | 100.0 | 19 | 4 | AAC93016 | Aac93016 C. cibari | |
| 20 | 19 | 100.0 | 19 | 4 | AAS08395 | Aas08395 Internal | |
| 21 | 19 | 100.0 | 19 | 4 | AAC91829 | Aac91829 C. cibari | |
| 22 | 19 | 100.0 | 19 | 4 | AAC91161 | Aac91161 Universal | |
| 23 | 19 | 100.0 | 19 | 6 | ABS70017 | Abs70017 Aspergill | |
| 24 | 19 | 100.0 | 19 | 6 | ABA94546 | Aba94546 Mycosphae | |
| 25 | 19 | 100.0 | 19 | 8 | ACC50003 | Acc50003 oligonucl | |
| 26 | 19 | 100.0 | 19 | 9 | ACC47145 | Acc47145 Nucleotid | |
| 27 | 19 | 100.0 | 19 | 10 | ABV77013 | Abv77013 Primer IT | |
| 28 | 19 | 100.0 | 19 | 12 | ADH61955 | Adh61955 Panellus | |
| 29 | 19 | 100.0 | 19 | 12 | ADK23612 | Adk23612 Fungal un | |
| 30 | 19 | 100.0 | 19 | 12 | ADM56196 | Adm56196 Myrotheci | |
| 31 | 19 | 100.0 | 19 | 12 | ADN61575 | Adn61575 Fungi, oo | |
| c | 32 | 18 | 94.7 | 18 | 12 | ADJ57011 | Adj57011 Primer 18 |
| | 33 | 18 | 94.7 | 19 | 4 | AAH03087 | Aah03087 Microorga |
| | 34 | 18 | 94.7 | 19 | 9 | ADA27511 | Ada27511 Micoorgan |
| c | 35 | 17 | 89.5 | 19 | 13 | ADR69344 | Adr69344 Novel mol |
| c | 36 | 16 | 84.2 | 16 | 2 | AAQ50414 | Aaq50414 Primer 2 |
| c | 37 | 16 | 84.2 | 16 | 2 | AAT02856 | Aat02856 Fungus-de |
| c | 38 | 16 | 84.2 | 17 | 2 | AAX69376 | Aax69376 Human flt |
| c | 39 | 16 | 84.2 | 17 | 2 | AAX69375 | Aax69375 Human flt |
| c | 40 | 16 | 84.2 | 19 | 10 | ADF35943 | Adf35943 Human VEG |
| 41 | 16 | 84.2 | 19 | 10 | ADF36370 | Adf36370 Human VEG | |
| c | 42 | 14 | 73.7 | 18 | 2 | AAV54103 | Aav54103 Nucleotid |
| c | 43 | 14 | 73.7 | 18 | 2 | AAV60124 | Aav60124 PCR prime |
| c | 44 | 14 | 73.7 | 18 | 2 | AAV61685 | Aav61685 Fusarium |
| | 45 | 13 | 68.4 | 13 | 2 | AAV09940 | Aav09940 Nucleotid |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 14:43:20 ; Search time 124 Seconds
(without alignments)
250.720 Million cell
updates/sec

Title: US-10-623-880-1

Perfect score: 19

Sequence: 1 tccgttagtgaacctgcgg 19

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

word size : 0

Total number of hits satisfying chosen parameters: 276054

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:/*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:/*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:/*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:/*
5: /cgn2_6/ptodata/1/ina/PECTUS_COMB.seq:/*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match | Length | DB | ID | Description |
|------------|-------|---------|-------|--------|----|----|-------------|
|------------|-------|---------|-------|--------|----|----|-------------|

| | | | | | | | |
|----|----|-------|----|---|------------------|--|--------------------|
| 1 | 19 | 100.0 | 19 | 1 | US-08-065-845-1 | | Sequence 1, Appli |
| 2 | 19 | 100.0 | 19 | 1 | US-08-233-608-38 | | Sequence 38, Appli |
| 3 | 19 | 100.0 | 19 | 1 | US-08-429-523-1 | | Sequence 1, Appli |
| 4 | 19 | 100.0 | 19 | 1 | US-08-429-532-1 | | Sequence 1, Appli |
| 5 | 19 | 100.0 | 19 | 1 | US-08-429-522-1 | | Sequence 1, Appli |
| 6 | 19 | 100.0 | 19 | 1 | US-08-429-520-1 | | Sequence 1, Appli |
| 7 | 19 | 100.0 | 19 | 1 | US-08-742-023-9 | | Sequence 9, Appli |
| 8 | 19 | 100.0 | 19 | 1 | US-08-887-480-38 | | Sequence 38, Appli |
| 9 | 19 | 100.0 | 19 | 1 | US-08-905-314A-1 | | Sequence 1, Appli |
| 10 | 19 | 100.0 | 19 | 2 | US-08-722-187-38 | | Sequence 38, Appli |
| 11 | 19 | 100.0 | 19 | 3 | US-08-968-505-9 | | Sequence 9, Appli |
| 12 | 19 | 100.0 | 19 | 3 | US-09-258-967-1 | | Sequence 1, Appli |
| 13 | 19 | 100.0 | 19 | 3 | US-09-269-136B-1 | | Sequence 1, Appli |
| 14 | 19 | 100.0 | 19 | 3 | US-09-635-747-1 | | Sequence 1, Appli |
| 15 | 19 | 100.0 | 19 | 3 | US-09-026-601-1 | | Sequence 1, Appli |

Untitled

| | | | | | | |
|------|----|-------|----|---|---------------------|--------------------|
| 16 | 19 | 100.0 | 19 | 3 | US-09-673-298-1 | Sequence 1, Appli |
| 17 | 19 | 100.0 | 19 | 4 | US-09-481-293-1 | Sequence 1, Appli |
| 18 | 19 | 100.0 | 19 | 4 | US-09-939-379B-1 | Sequence 1, Appli |
| 19 | 19 | 100.0 | 19 | 4 | US-09-961-663-1 | Sequence 1, Appli |
| 20 | 19 | 100.0 | 19 | 5 | PCT-US95-04712-38 | Sequence 38, Appli |
| 21 | 18 | 94.7 | 19 | 3 | US-09-311-260-111 | Sequence 111, App |
| c 22 | 16 | 84.2 | 17 | 3 | US-08-584-040-2125 | Sequence 2125, Ap |
| c 23 | 16 | 84.2 | 17 | 3 | US-08-584-040-2126 | Sequence 2126, Ap |
| c 24 | 16 | 84.2 | 17 | 4 | US-09-371-772B-670 | Sequence 670, App |
| c 25 | 16 | 84.2 | 17 | 4 | US-09-371-772B-671 | Sequence 671, App |
| c 26 | 16 | 84.2 | 17 | 4 | US-09-685-664B-670 | Sequence 670, App |
| c 27 | 16 | 84.2 | 17 | 4 | US-09-685-664B-671 | Sequence 671, App |
| c 28 | 15 | 78.9 | 17 | 4 | US-09-371-772B-4998 | Sequence 4998, App |
| 29 | 13 | 68.4 | 13 | 2 | US-08-883-920-6 | Sequence 6, Appli |
| c 30 | 13 | 68.4 | 17 | 4 | US-09-371-772B-4999 | Sequence 4999, Ap |
| c 31 | 12 | 63.2 | 17 | 4 | US-09-371-772B-4997 | Sequence 4997, Ap |
| c 32 | 12 | 63.2 | 17 | 4 | US-09-371-772B-5000 | Sequence 5000, Ap |
| 33 | 12 | 63.2 | 18 | 4 | US-09-856-662-74 | Sequence 74, Appli |
| 34 | 12 | 63.2 | 19 | 1 | US-08-796-883-13 | Sequence 13, Appli |
| 35 | 12 | 63.2 | 19 | 2 | US-08-531-864-13 | Sequence 13, Appli |
| 36 | 12 | 63.2 | 19 | 2 | US-08-373-636C-13 | Sequence 13, Appli |
| 37 | 12 | 63.2 | 19 | 3 | US-08-602-506A-13 | Sequence 13, Appli |
| 38 | 12 | 63.2 | 19 | 3 | US-09-266-294-13 | Sequence 13, Appli |
| 39 | 12 | 63.2 | 19 | 3 | US-09-179-281-13 | Sequence 13, Appli |
| 40 | 12 | 63.2 | 19 | 4 | US-09-747-391-1 | Sequence 1, Appli |
| 41 | 12 | 63.2 | 19 | 4 | US-09-747-391-119 | Sequence 119, App |
| c 42 | 11 | 57.9 | 16 | 4 | US-09-371-772B-5911 | Sequence 5911, Ap |
| c 43 | 11 | 57.9 | 17 | 3 | US-08-584-040-2127 | Sequence 2127, Ap |
| c 44 | 11 | 57.9 | 17 | 4 | US-09-371-772B-672 | Sequence 672, App |
| c 45 | 11 | 57.9 | 17 | 4 | US-09-685-664B-672 | Sequence 672, App |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 14:39:49 ; Search time 605 Seconds
(without alignments)
209.238 Million cell
updates/sec

Title: US-10-623-880-1
Perfect score: 19
Sequence: 1 tccgttaggtgaacctgcgg 19

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7389322 seqs, 3331285599 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1397872

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:/*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:/*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:/*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:/*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:/*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:/*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:/*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:/*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:/*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:/*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:/*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:/*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:/*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:/*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:/*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:/*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:/*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:/*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:/*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:/*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:/*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:/*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:/*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:/*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:/*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Untitled

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---------------|-------|---------------------|--------|----|---------------------|--------------------|
| 1 | 19 | 100.0 | 19 | 9 | US-09-961-663-1 | Sequence 1, Appli |
| 2 | 19 | 100.0 | 19 | 10 | US-09-939-379B-1 | Sequence 1, Appli |
| 3 | 19 | 100.0 | 19 | 10 | US-09-961-755A-9 | Sequence 9, Appli |
| 4 | 19 | 100.0 | 19 | 14 | US-10-199-559-1 | Sequence 1, Appli |
| 5 | 19 | 100.0 | 19 | 17 | US-10-623-880-1 | Sequence 1, Appli |
| 6 | 19 | 100.0 | 19 | 19 | US-10-468-250A-145 | Sequence 145, App |
| 7 | 19 | 100.0 | 19 | 20 | US-10-773-904-9 | Sequence 9, Appli |
| 8 | 19 | 100.0 | 19 | 20 | US-10-773-905-9 | Sequence 9, Appli |
| 9 | 19 | 100.0 | 19 | 22 | US-10-757-093-24 | Sequence 24, Appli |
| 10 | 19 | 100.0 | 19 | 22 | US-10-514-861-31 | Sequence 31, Appli |
| 11 | 18 | 94.7 | 19 | 10 | US-09-802-110B-111 | Sequence 111, App |
| c 12 | 16 | 84.2 | 17 | 18 | US-10-138-674-670 | Sequence 670, App |
| c 13 | 16 | 84.2 | 17 | 18 | US-10-138-674-671 | Sequence 671, App |
| c 14 | 16 | 84.2 | 17 | 19 | US-10-287-949A-670 | Sequence 670, App |
| c 15 | 16 | 84.2 | 17 | 19 | US-10-287-949A-671 | Sequence 671, App |
| c 16 | 16 | 84.2 | 19 | 19 | US-10-665-951-232 | Sequence 232, App |
| 17 | 16 | 84.2 | 19 | 19 | US-10-665-951-659 | Sequence 659, App |
| c 18 | 16 | 84.2 | 19 | 21 | US-10-758-155-232 | Sequence 232, App |
| 19 | 16 | 84.2 | 19 | 21 | US-10-758-155-659 | Sequence 659, App |
| c 20 | 16 | 84.2 | 19 | 22 | US-10-831-620-232 | Sequence 232, App |
| 21 | 16 | 84.2 | 19 | 22 | US-10-831-620-659 | Sequence 659, App |
| c 22 | 16 | 84.2 | 19 | 22 | US-10-844-076-232 | Sequence 232, App |
| 23 | 16 | 84.2 | 19 | 22 | US-10-844-076-659 | Sequence 659, App |
| c 24 | 15 | 78.9 | 17 | 18 | US-10-138-674-4998 | Sequence 4998, Ap |
| c 25 | 15 | 78.9 | 17 | 19 | US-10-287-949A-4998 | Sequence 4998, Ap |
| c 26 | 15 | 78.9 | 17 | 20 | US-10-712-633-935 | Sequence 935, App |
| c 27 | 14 | 73.7 | 17 | 18 | US-10-138-674-7830 | Sequence 7830, Ap |
| c 28 | 14 | 73.7 | 17 | 19 | US-10-287-949A-7830 | Sequence 7830, Ap |
| c 29 | 14 | 73.7 | 17 | 20 | US-10-712-633-934 | Sequence 934, App |
| c 30 | 13 | 68.4 | 17 | 18 | US-10-138-674-4999 | Sequence 4999, Ap |
| c 31 | 13 | 68.4 | 17 | 19 | US-10-287-949A-4999 | Sequence 4999, Ap |
| c 32 | 12 | 63.2 | 17 | 18 | US-10-138-674-4997 | Sequence 4997, Ap |
| c 33 | 12 | 63.2 | 17 | 18 | US-10-138-674-5000 | Sequence 5000, Ap |
| c 34 | 12 | 63.2 | 17 | 19 | US-10-287-949A-4997 | Sequence 4997, Ap |
| c 35 | 12 | 63.2 | 17 | 19 | US-10-287-949A-5000 | Sequence 5000, Ap |
| c 36 | 12 | 63.2 | 18 | 9 | US-09-875-338-88 | Sequence 88, Appl |
| c 37 | 12 | 63.2 | 18 | 14 | US-10-077-023-88 | Sequence 88, Appl |
| 38 | 12 | 63.2 | 18 | 21 | US-10-920-184-74 | Sequence 74, Appl |
| 39 | 12 | 63.2 | 19 | 16 | US-10-133-779-1 | Sequence 1, Appli |
| 40 | 12 | 63.2 | 19 | 16 | US-10-133-779-119 | Sequence 119, App |
| c 41 | 11 | 57.9 | 16 | 18 | US-10-138-674-5911 | Sequence 5911, Ap |
| c 42 | 11 | 57.9 | 16 | 19 | US-10-287-949A-5911 | Sequence 5911, Ap |
| c 43 | 11 | 57.9 | 17 | 18 | US-10-138-674-672 | Sequence 672, App |
| c 44 | 11 | 57.9 | 17 | 19 | US-10-287-949A-672 | Sequence 672, App |
| c 45 | 11 | 57.9 | 17 | 20 | US-10-712-633-936 | Sequence 936, App |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 12:53:08 ; Search time 3022 Seconds
(without alignments)
239.319 Million cell

updates/sec

Title: US-10-623-880-1

Perfect score: 19

Sequence: 1 tccgttaggtgaacctgcgg 19

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9364

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | % Length | DB | ID | Description |
|------------|-------|-------------|----------|----|----------|--------------------|
| c 1 | 9 | 47.4 | 10 | 9 | CL438130 | CL438130 PST6863-N |
| c 2 | 8 | 42.1 | 19 | 2 | AW246513 | AW246513 2821739.3 |
| c 3 | 8 | 42.1 | 19 | 8 | AZ644418 | AZ644418 1M0508B20 |
| c 4 | 8 | 42.1 | 19 | 8 | AZ835621 | AZ835621 2M0129L21 |
| c 5 | 7 | 36.8 | 13 | 9 | AJ587972 | AJ587972 Arabidops |
| c 6 | 7 | 36.8 | 15 | 6 | CA851407 | CA851407 D13D09_G0 |
| c 7 | 7 | 36.8 | 16 | 9 | CL423510 | CL423510 01S0557-0 |
| c 8 | 7 | 36.8 | 17 | 1 | AJ654055 | AJ654055 AJ654055 |
| c 9 | 7 | 36.8 | 18 | 9 | AJ594669 | AJ594669 Arabidops |
| c 10 | 7 | 36.8 | 19 | 7 | C0791279 | C0791279 NT012A_A0 |
| c 11 | 7 | 36.8 | 19 | 8 | AZ331326 | AZ331326 1M0059B15 |
| c 12 | 7 | 36.8 | 19 | 8 | AZ345449 | AZ345449 1M0080I08 |

Untitled

| | | | | | | | | |
|---|----|---|------|----|---|----------|----------|-----------|
| c | 13 | 7 | 36.8 | 19 | 8 | AZ345511 | AZ345511 | 1M0080J01 |
| c | 14 | 7 | 36.8 | 19 | 8 | AZ345536 | AZ345536 | 1M0080006 |
| c | 15 | 7 | 36.8 | 19 | 8 | AZ345572 | AZ345572 | 1M0080J17 |
| c | 16 | 7 | 36.8 | 19 | 8 | AZ346709 | AZ346709 | 1M0082M06 |
| c | 17 | 7 | 36.8 | 19 | 8 | AZ346710 | AZ346710 | 1M0082N01 |
| c | 18 | 7 | 36.8 | 19 | 8 | AZ368837 | AZ368837 | 1M0119A11 |
| c | 19 | 7 | 36.8 | 19 | 8 | AZ447223 | AZ447223 | 1M0244H13 |
| c | 20 | 7 | 36.8 | 19 | 8 | AZ447247 | AZ447247 | 1M0244G19 |
| | 21 | 7 | 36.8 | 19 | 8 | AZ477382 | AZ477382 | 1M0296P16 |
| c | 22 | 7 | 36.8 | 19 | 8 | AZ482658 | AZ482658 | 1M0307L16 |
| | 23 | 7 | 36.8 | 19 | 8 | AZ500335 | AZ500335 | 1M0338G07 |
| c | 24 | 7 | 36.8 | 19 | 8 | AZ510096 | AZ510096 | 1M0354B22 |
| c | 25 | 7 | 36.8 | 19 | 8 | AZ510106 | AZ510106 | 1M0354E19 |
| c | 26 | 7 | 36.8 | 19 | 8 | AZ634762 | AZ634762 | 1M0490C18 |
| c | 27 | 7 | 36.8 | 19 | 8 | AZ638980 | AZ638980 | 1M0499L08 |
| | 28 | 7 | 36.8 | 19 | 8 | AZ651870 | AZ651870 | 1M0522M15 |
| | 29 | 7 | 36.8 | 19 | 8 | AZ655467 | AZ655467 | 1M0530O17 |
| c | 30 | 7 | 36.8 | 19 | 8 | AZ827164 | AZ827164 | 2M0103M22 |
| c | 31 | 6 | 31.6 | 10 | 9 | AJ598893 | AJ598893 | Arabidops |
| c | 32 | 6 | 31.6 | 10 | 9 | CL437066 | CL437066 | PST4433-N |
| c | 33 | 6 | 31.6 | 11 | 1 | AJ663404 | AJ663404 | |
| c | 34 | 6 | 31.6 | 11 | 4 | BG927896 | BG927896 | HNC45-1-D |
| | 35 | 6 | 31.6 | 11 | 5 | BQ592717 | BQ592717 | E012124-0 |
| c | 36 | 6 | 31.6 | 11 | 5 | BQ595402 | BQ595402 | E012693-0 |
| | 37 | 6 | 31.6 | 11 | 9 | CL437175 | CL437175 | PST4640-N |
| | 38 | 6 | 31.6 | 12 | 1 | AJ747414 | AJ747414 | AJ747414 |
| | 39 | 6 | 31.6 | 12 | 1 | AJ747580 | AJ747580 | AJ747580 |
| | 40 | 6 | 31.6 | 13 | 1 | AJ679030 | AJ679030 | AJ679030 |
| | 41 | 6 | 31.6 | 13 | 8 | BH170808 | BH170808 | SALK_0033 |
| | 42 | 6 | 31.6 | 13 | 9 | AJ588255 | AJ588255 | Arabidops |
| | 43 | 6 | 31.6 | 13 | 9 | AJ594173 | AJ594173 | Arabidops |
| | 44 | 6 | 31.6 | 13 | 9 | AJ598721 | AJ598721 | Arabidops |
| c | 45 | 6 | 31.6 | 14 | 1 | AJ655566 | AJ655566 | AJ655566 |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 15:40:55 ; Search time 1830 Seconds
(without alignments)
529.565 Million cell
updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttctt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 790860

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | % Description | |
|---------------|-------|----------------|--------|----|----------|---------------|-----------|
| | | | | | | | |
| 1 | 20 | 100.0 | 20 | 6 | AR429595 | AR429595 | Sequence |
| 2 | 20 | 100.0 | 20 | 6 | AX592693 | AX592693 | Sequence |
| 3 | 13 | 65.0 | 16 | 6 | AR429593 | AR429593 | Sequence |
| 4 | 13 | 65.0 | 16 | 6 | AX592691 | AX592691 | Sequence |
| c 5 | 12 | 60.0 | 20 | 6 | AR116448 | AR116448 | Sequence |
| c 6 | 12 | 60.0 | 20 | 6 | AX020008 | AX020008 | Sequence |
| c 7 | 12 | 60.0 | 20 | 6 | BD074605 | BD074605 | Antisence |

| Untitled | | | | | | |
|----------|----|----|------|----|---|--------------------|
| c | 8 | 11 | 55.0 | 17 | 6 | AR192354 Sequence |
| c | 9 | 11 | 55.0 | 17 | 6 | AR326223 Sequence |
| c | 10 | 11 | 55.0 | 17 | 6 | AX757656 Sequence |
| c | 11 | 11 | 55.0 | 19 | 6 | AX298780 Sequence |
| c | 12 | 11 | 55.0 | 20 | 6 | AX111309 Sequence |
| c | 13 | 11 | 55.0 | 20 | 6 | AX474051 Sequence |
| c | 14 | 10 | 50.0 | 11 | 6 | AR301743 Sequence |
| c | 15 | 10 | 50.0 | 11 | 6 | AX623235 Sequence |
| c | 16 | 10 | 50.0 | 11 | 6 | AX630656 Sequence |
| c | 17 | 10 | 50.0 | 11 | 6 | BD124493 Composite |
| c | 18 | 10 | 50.0 | 17 | 6 | AR186718 Sequence |
| c | 19 | 10 | 50.0 | 17 | 6 | AR323349 Sequence |
| c | 20 | 10 | 50.0 | 17 | 6 | AX214909 Sequence |
| c | 21 | 10 | 50.0 | 17 | 6 | AX214910 Sequence |
| c | 22 | 10 | 50.0 | 17 | 6 | AX214911 Sequence |
| c | 23 | 10 | 50.0 | 17 | 6 | AX214912 Sequence |
| c | 24 | 10 | 50.0 | 17 | 6 | AX215791 Sequence |
| c | 25 | 10 | 50.0 | 17 | 6 | AX216769 Sequence |
| c | 26 | 10 | 50.0 | 17 | 6 | AX217116 Sequence |
| c | 27 | 10 | 50.0 | 17 | 6 | AX756835 Sequence |
| c | 28 | 10 | 50.0 | 17 | 6 | AX761071 Sequence |
| c | 29 | 10 | 50.0 | 18 | 6 | AR175669 Sequence |
| c | 30 | 10 | 50.0 | 18 | 6 | BD224873 Antisense |
| c | 31 | 10 | 50.0 | 18 | 6 | AR195245 Sequence |
| c | 32 | 10 | 50.0 | 18 | 6 | AR211095 Sequence |
| c | 33 | 10 | 50.0 | 18 | 6 | AR222327 Sequence |
| c | 34 | 10 | 50.0 | 18 | 6 | AR241446 Sequence |
| c | 35 | 10 | 50.0 | 18 | 6 | AR298065 Sequence |
| c | 36 | 10 | 50.0 | 18 | 6 | AX705641 Sequence |
| c | 37 | 10 | 50.0 | 18 | 6 | AX705643 Sequence |
| c | 38 | 10 | 50.0 | 18 | 6 | AX822833 Sequence |
| c | 39 | 10 | 50.0 | 18 | 6 | AX826473 Sequence |
| c | 40 | 10 | 50.0 | 18 | 6 | BD014812 Modulator |
| c | 41 | 10 | 50.0 | 20 | 4 | L24236 Dog (Clone: |
| c | 42 | 10 | 50.0 | 20 | 6 | AR092413 Sequence |
| c | 43 | 10 | 50.0 | 20 | 6 | AR116535 Sequence |
| c | 44 | 10 | 50.0 | 20 | 6 | AR233669 Sequence |
| c | 45 | 10 | 50.0 | 20 | 6 | AR293020 Sequence |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 14:50:20 ; Search time 415 Seconds
(without alignments)
285.289 Million cell

updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2207178

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | % | Length | DB | ID | Description |
|---------------|-------|----------------|---|--------|----|----------|--------------------|
| <hr/> | | | | | | | |
| 1 | 20 | 100.0 | | 20 | 10 | ABV77037 | Abv77037 Primer Vc |
| 2 | 13 | 65.0 | | 16 | 10 | ABV77035 | Abv77035 Primer Vc |
| c 3 | 12 | 60.0 | | 20 | 2 | AAZ00572 | Aaz00572 Human GPC |
| c 4 | 12 | 60.0 | | 20 | 2 | AAX29329 | Aax29329 JNK2-spec |
| c 5 | 12 | 60.0 | | 20 | 3 | AAC62872 | Aac62872 JNK antis |
| c 6 | 12 | 60.0 | | 20 | 8 | ADA26576 | Ada26576 Human Jun |
| c 7 | 12 | 60.0 | | 20 | 10 | ADC55474 | Adc55474 Primer #3 |
| c 8 | 12 | 60.0 | | 20 | 12 | ADN48318 | Adn48318 Human Jun |

| Untitled | | | | | | |
|----------|----|------|----|----|----------|--------------------|
| c 9 | 11 | 55.0 | 13 | 5 | ABC59176 | Abc59176 Oligonucl |
| c 10 | 11 | 55.0 | 13 | 5 | ABC59175 | Abc59175 Oligonucl |
| c 11 | 11 | 55.0 | 13 | 5 | ABC59174 | Abc59174 Oligonucl |
| c 12 | 11 | 55.0 | 13 | 5 | ABC59177 | Abc59177 Oligonucl |
| c 13 | 11 | 55.0 | 17 | 2 | AAX75092 | Aax75092 Mouse flt |
| c 14 | 11 | 55.0 | 17 | 2 | AAV95270 | Aav95270 Human c-f |
| c 15 | 11 | 55.0 | 17 | 10 | ADB40654 | Adb40654 Tumour su |
| c 16 | 11 | 55.0 | 18 | 2 | AAV51658 | Aav51658 Zea mays |
| c 17 | 11 | 55.0 | 19 | 6 | AAS97804 | Aas97804 Murine SA |
| c 18 | 11 | 55.0 | 19 | 12 | ADM16144 | Adm16144 Murine SA |
| c 19 | 11 | 55.0 | 20 | 4 | AAH02049 | Aah02049 gyrA resi |
| c 20 | 11 | 55.0 | 20 | 6 | ABN89794 | Abn89794 Human ABC |
| c 21 | 10 | 50.0 | 10 | 3 | AAZ84641 | Aaz84641 Metastati |
| c 22 | 10 | 50.0 | 10 | 6 | ABL01198 | Ab101198 Human AKR |
| c 23 | 10 | 50.0 | 11 | 2 | AAZ19014 | Aaz19014 Murine MR |
| c 24 | 10 | 50.0 | 11 | 6 | ABV62490 | Abv62490 Human ski |
| c 25 | 10 | 50.0 | 11 | 6 | ABV69911 | Abv69911 Human ski |
| c 26 | 10 | 50.0 | 13 | 5 | ABF30081 | Abf30081 Oligonucl |
| c 27 | 10 | 50.0 | 13 | 5 | ABF30080 | Abf30080 Oligonucl |
| c 28 | 10 | 50.0 | 15 | 4 | AAF45167 | Aaf45167 IGFBP2 o1 |
| c 29 | 10 | 50.0 | 15 | 4 | AAF45166 | Aaf45166 IGFBP2 o1 |
| c 30 | 10 | 50.0 | 15 | 4 | AAF45162 | Aaf45162 IGFBP2 o1 |
| c 31 | 10 | 50.0 | 15 | 4 | AAF45163 | Aaf45163 IGFBP2 o1 |
| c 32 | 10 | 50.0 | 15 | 4 | AAF45164 | Aaf45164 IGFBP2 o1 |
| c 33 | 10 | 50.0 | 15 | 4 | AAF45165 | Aaf45165 IGFBP2 o1 |
| c 34 | 10 | 50.0 | 15 | 6 | ABL01152 | Ab101152 Human AKR |
| c 35 | 10 | 50.0 | 17 | 2 | AAX69456 | Aax69456 Human flt |
| c 36 | 10 | 50.0 | 17 | 4 | ABK01233 | Abk01233 Human NOG |
| c 37 | 10 | 50.0 | 17 | 4 | ABK00353 | Abk00353 Human NOG |
| c 38 | 10 | 50.0 | 17 | 4 | ABK02558 | Abk02558 Human NOG |
| c 39 | 10 | 50.0 | 17 | 4 | ABK00352 | Abk00352 Human NOG |
| c 40 | 10 | 50.0 | 17 | 4 | ABK02211 | Abk02211 Human NOG |
| c 41 | 10 | 50.0 | 17 | 4 | ABK00351 | Abk00351 Human NOG |
| c 42 | 10 | 50.0 | 17 | 4 | ABK00354 | Abk00354 Human NOG |
| c 43 | 10 | 50.0 | 17 | 10 | ADB44069 | Adb44069 Tumour su |
| c 44 | 10 | 50.0 | 17 | 10 | ADB39833 | Adb39833 Tumour su |
| c 45 | 10 | 50.0 | 18 | 2 | AAT16422 | Aat16422 Primer #1 |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 16:21:40 ; Search time 123 Seconds
(without alignments)
266.061 Million cell
updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 401682

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/1/ina/PECTUS_COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % | Query Match | Length | DB ID | Description |
|------------|-------|-------|-------------|--------|---------------------|--------------------|
| 1 | 20 | 100.0 | 20 | 4 | US-09-939-379B-27 | Sequence 27, Appl |
| 2 | 13 | 65.0 | 16 | 4 | US-09-939-379B-25 | Sequence 25, Appl |
| c 3 | 12 | 60.0 | 20 | 2 | US-08-910-629A-29 | Sequence 29, Appl |
| c 4 | 12 | 60.0 | 20 | 3 | US-09-287-796-29 | Sequence 29, Appl |
| c 5 | 12 | 60.0 | 20 | 3 | US-09-130-616-29 | Sequence 29, Appl |
| c 6 | 12 | 60.0 | 20 | 4 | US-09-774-809-29 | Sequence 29, Appl |
| c 7 | 11 | 55.0 | 17 | 3 | US-08-998-099-10 | Sequence 10, Appl |
| c 8 | 11 | 55.0 | 17 | 3 | US-08-584-040-7842 | Sequence 7842, Ap |
| c 9 | 11 | 55.0 | 17 | 4 | US-09-371-772B-3625 | Sequence 3625, Ap |
| c 10 | 11 | 55.0 | 17 | 4 | US-09-685-664B-3625 | Sequence 3625, Ap |
| 11 | 10 | 50.0 | 11 | 4 | US-09-249-155A-324 | Sequence 324, App |
| c 12 | 10 | 50.0 | 17 | 3 | US-08-584-040-2206 | Sequence 2206, App |
| c 13 | 10 | 50.0 | 17 | 4 | US-09-371-772B-751 | Sequence 751, App |
| c 14 | 10 | 50.0 | 17 | 4 | US-09-685-664B-751 | Sequence 751, App |
| 15 | 10 | 50.0 | 18 | 3 | US-08-485-942A-69 | Sequence 69, Appl |

Untitled

| | | | | | | |
|------|----|------|----|---|---------------------|-------------------|
| 16 | 10 | 50.0 | 18 | 3 | US-08-488-214A-69 | Sequence 69, Appl |
| 17 | 10 | 50.0 | 18 | 3 | US-08-488-208A-69 | Sequence 69, Appl |
| 18 | 10 | 50.0 | 18 | 3 | US-09-723-534-22 | Sequence 22, Appl |
| 19 | 10 | 50.0 | 18 | 3 | US-08-483-211A-69 | Sequence 69, Appl |
| 20 | 10 | 50.0 | 18 | 3 | US-08-488-223A-69 | Sequence 69, Appl |
| 21 | 10 | 50.0 | 18 | 3 | US-09-167-109-8 | Sequence 8, Appl |
| 22 | 10 | 50.0 | 18 | 3 | US-08-438-431A-69 | Sequence 69, Appl |
| 23 | 10 | 50.0 | 18 | 4 | US-08-488-225A-69 | Sequence 69, Appl |
| c 24 | 10 | 50.0 | 18 | 4 | US-09-422-978-9800 | Sequence 9800, Ap |
| 25 | 10 | 50.0 | 20 | 2 | US-09-289-368-84 | Sequence 84, Appl |
| 26 | 10 | 50.0 | 20 | 3 | US-09-287-796-116 | Sequence 116, App |
| 27 | 10 | 50.0 | 20 | 3 | US-09-130-616-116 | Sequence 116, App |
| c 28 | 10 | 50.0 | 20 | 3 | US-09-360-416-31 | Sequence 31, Appl |
| 29 | 10 | 50.0 | 20 | 4 | US-09-422-978-4755 | Sequence 4755, Ap |
| c 30 | 10 | 50.0 | 20 | 4 | US-09-198-452A-2980 | Sequence 2980, Ap |
| c 31 | 10 | 50.0 | 20 | 4 | US-09-198-452A-5733 | Sequence 5733, Ap |
| c 32 | 10 | 50.0 | 20 | 4 | US-09-780-172-68 | Sequence 68, Appl |
| 33 | 10 | 50.0 | 20 | 4 | US-09-774-809-116 | Sequence 116, App |
| 34 | 9 | 45.0 | 10 | 3 | US-08-482-073-16 | Sequence 16, Appl |
| c 35 | 9 | 45.0 | 12 | 2 | US-08-173-489C-340 | Sequence 340, App |
| 36 | 9 | 45.0 | 12 | 3 | US-09-281-418-125 | Sequence 125, App |
| c 37 | 9 | 45.0 | 12 | 4 | US-09-497-855A-50 | Sequence 50, Appl |
| c 38 | 9 | 45.0 | 15 | 2 | US-08-765-176-1 | Sequence 1, Appl |
| c 39 | 9 | 45.0 | 15 | 2 | US-08-585-684B-2085 | Sequence 2085, Ap |
| c 40 | 9 | 45.0 | 15 | 3 | US-09-038-073-2085 | Sequence 2085, Ap |
| 41 | 9 | 45.0 | 15 | 3 | US-09-081-646-202 | Sequence 202, App |
| 42 | 9 | 45.0 | 15 | 3 | US-09-081-646-743 | Sequence 743, App |
| c 43 | 9 | 45.0 | 15 | 3 | US-09-423-233-40 | Sequence 40, Appl |
| c 44 | 9 | 45.0 | 16 | 1 | US-08-233-030-52 | Sequence 52, Appl |
| 45 | 9 | 45.0 | 16 | 4 | US-09-371-772B-5653 | Sequence 5653, Ap |

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 16:23:55 ; Search time 602 Seconds
(without alignments)
221.348 Million cell

updates/sec

Title: US-10-623-880-27

Perfect score: 20

Sequence: 1 ccgggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7389322 seqs, 3331285599 residues

word size : 0

Total number of hits satisfying chosen parameters: 1761270

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*

24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Page 1

Untitled

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---------------|-------|---------------------|--------|----|-----------------------|-------------------|
| 1 | 20 | 100.0 | 20 | 10 | US-09-939-379B-27 | Sequence 27, Appl |
| 2 | 20 | 100.0 | 20 | 14 | US-10-199-559-27 | Sequence 27, Appl |
| 3 | 20 | 100.0 | 20 | 17 | US-10-623-880-27 | Sequence 27, Appl |
| 4 | 13 | 65.0 | 16 | 10 | US-09-939-379B-25 | Sequence 25, Appl |
| 5 | 13 | 65.0 | 16 | 14 | US-10-199-559-25 | Sequence 25, Appl |
| 6 | 13 | 65.0 | 16 | 17 | US-10-623-880-25 | Sequence 25, Appl |
| c 7 | 12 | 60.0 | 20 | 10 | US-09-774-809-29 | Sequence 29, Appl |
| c 8 | 12 | 60.0 | 20 | 17 | US-10-345-444B-29 | Sequence 29, Appl |
| c 9 | 11 | 55.0 | 13 | 20 | US-10-257-017B-59191 | Sequence 59191, A |
| c 10 | 11 | 55.0 | 13 | 20 | US-10-257-017B-59192 | Sequence 59192, A |
| c 11 | 11 | 55.0 | 13 | 20 | US-10-257-017B-59193 | Sequence 59193, A |
| c 12 | 11 | 55.0 | 13 | 20 | US-10-257-017B-59194 | Sequence 59194, A |
| c 13 | 11 | 55.0 | 17 | 18 | US-10-138-674-3625 | Sequence 3625, Ap |
| c 14 | 11 | 55.0 | 17 | 19 | US-10-287-949A-3625 | Sequence 3625, Ap |
| c 15 | 11 | 55.0 | 19 | 18 | US-10-280-183A-414 | Sequence 414, App |
| c 16 | 11 | 55.0 | 20 | 14 | US-10-005-338B-205 | Sequence 205, App |
| 17 | 11 | 55.0 | 20 | 20 | US-10-767-441-11 | Sequence 11, Appl |
| 18 | 10 | 50.0 | 11 | 17 | US-10-314-322-324 | Sequence 324, App |
| 19 | 10 | 50.0 | 13 | 20 | US-10-257-017B-130077 | Sequence 130077, |
| c 20 | 10 | 50.0 | 13 | 20 | US-10-257-017B-130078 | Sequence 130078, |
| 21 | 10 | 50.0 | 17 | 10 | US-09-780-533A-351 | Sequence 351, App |
| 22 | 10 | 50.0 | 17 | 10 | US-09-780-533A-352 | Sequence 352, App |
| 23 | 10 | 50.0 | 17 | 10 | US-09-780-533A-353 | Sequence 353, App |
| 24 | 10 | 50.0 | 17 | 10 | US-09-780-533A-354 | Sequence 354, App |
| 25 | 10 | 50.0 | 17 | 10 | US-09-780-533A-1233 | Sequence 1233, Ap |
| 26 | 10 | 50.0 | 17 | 10 | US-09-780-533A-2211 | Sequence 2211, Ap |
| 27 | 10 | 50.0 | 17 | 10 | US-09-780-533A-2558 | Sequence 2558, Ap |
| c 28 | 10 | 50.0 | 17 | 18 | US-10-138-674-751 | Sequence 751, App |
| c 29 | 10 | 50.0 | 17 | 18 | US-10-138-674-7881 | Sequence 7881, Ap |
| c 30 | 10 | 50.0 | 17 | 19 | US-10-287-949A-751 | Sequence 751, App |
| c 31 | 10 | 50.0 | 17 | 19 | US-10-287-949A-7881 | Sequence 7881, Ap |
| c 32 | 10 | 50.0 | 17 | 20 | US-10-712-633-1013 | Sequence 1013, Ap |
| 33 | 10 | 50.0 | 18 | 9 | US-09-736-084-69 | Sequence 69, Appl |
| 34 | 10 | 50.0 | 18 | 14 | US-10-067-125-8 | Sequence 8, Appl |
| c 35 | 10 | 50.0 | 18 | 17 | US-10-349-143-9800 | Sequence 9800, Ap |
| 36 | 10 | 50.0 | 18 | 20 | US-10-730-488-69 | Sequence 69, Appl |
| 37 | 10 | 50.0 | 18 | 21 | US-10-486-319A-310 | Sequence 310, App |
| c 38 | 10 | 50.0 | 18 | 21 | US-10-486-319A-312 | Sequence 312, App |
| c 39 | 10 | 50.0 | 19 | 19 | US-10-665-951-251 | Sequence 251, App |
| 40 | 10 | 50.0 | 19 | 19 | US-10-665-951-678 | Sequence 678, App |
| 41 | 10 | 50.0 | 19 | 21 | US-10-920-608-15 | Sequence 15, Appl |
| c 42 | 10 | 50.0 | 19 | 21 | US-10-758-155-251 | Sequence 251, App |
| 43 | 10 | 50.0 | 19 | 21 | US-10-758-155-678 | Sequence 678, App |
| 44 | 10 | 50.0 | 19 | 21 | US-10-652-791-6 | Sequence 6, Appl |
| c 45 | 10 | 50.0 | 19 | 21 | US-10-652-791-95 | Sequence 95, Appl |

Untitled
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2005, 16:11:25 ; Search time 3007 Seconds
(without alignments)
253.171 Million cell

updates/sec

Title: US-10-623-880-27
Perfect score: 20
Sequence: 1 ccgggcgagggatttcttt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

word size : 0

Total number of hits satisfying chosen parameters: 12452

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | % Length | DB | ID | Description |
|------------|-------|-------------|----------|----|----------|--------------------|
| 1 | 9 | 45.0 | 15 | 7 | CF303956 | CF303956 ABF1--03- |
| 2 | 9 | 45.0 | 19 | 7 | C0783722 | C0783722 BL018D_B0 |
| 3 | 9 | 45.0 | 20 | 7 | CF306120 | CF306120 HDA1--02- |
| 4 | 9 | 45.0 | 20 | 8 | AZ339855 | AZ339855 1M0071E03 |
| 5 | 8 | 40.0 | 10 | 9 | CL437947 | CL437947 PST6577-N |
| 6 | 8 | 40.0 | 11 | 7 | CF304450 | CF304450 ABF1--05- |
| c 7 | 8 | 40.0 | 16 | 5 | BQ588093 | BQ588093 E012336-0 |
| c 8 | 8 | 40.0 | 18 | 6 | CD530428 | CD530428 06D22 Ara |
| c 9 | 8 | 40.0 | 18 | 9 | AJ587746 | AJ587746 Arabidops |
| 10 | 8 | 40.0 | 19 | 1 | AI027323 | AI027323 ow46a07.s |
| 11 | 8 | 40.0 | 19 | 1 | AI371092 | AI371092 ta07g09.x |
| 12 | 8 | 40.0 | 19 | 8 | AZ345499 | AZ345499 1M0080F06 |

Untitled

| | | | | | | | | |
|---|----|---|------|----|---|----------|----------|-----------|
| c | 13 | 8 | 40.0 | 19 | 8 | AZ418201 | AZ418201 | 1M0194M12 |
| | 14 | 8 | 40.0 | 19 | 8 | AZ440413 | AZ440413 | 1M0231A01 |
| | 15 | 8 | 40.0 | 19 | 8 | AZ786336 | AZ786336 | 2M0031H17 |
| | 16 | 8 | 40.0 | 19 | 8 | AZ839439 | AZ839439 | 2M0135L06 |
| c | 17 | 8 | 40.0 | 19 | 8 | AZ874072 | AZ874072 | 2M0188M06 |
| c | 18 | 8 | 40.0 | 19 | 8 | AZ954943 | AZ954943 | 2M0220P16 |
| c | 19 | 8 | 40.0 | 19 | 9 | CL657902 | CL657902 | PRI012d_D |
| | 20 | 8 | 40.0 | 20 | 8 | AZ782717 | AZ782717 | 2M0023N21 |
| c | 21 | 8 | 40.0 | 20 | 8 | AZ796553 | AZ796553 | 2M0052P15 |
| | 22 | 7 | 35.0 | 12 | 9 | AJ593912 | AJ593912 | Arabidops |
| | 23 | 7 | 35.0 | 12 | 9 | AJ594491 | AJ594491 | Arabidops |
| | 24 | 7 | 35.0 | 13 | 1 | AJ666341 | AJ666341 | AJ666341 |
| | 25 | 7 | 35.0 | 13 | 9 | AJ590284 | AJ590284 | Arabidops |
| | 26 | 7 | 35.0 | 13 | 9 | AJ592721 | AJ592721 | Arabidops |
| | 27 | 7 | 35.0 | 13 | 9 | AJ593606 | AJ593606 | Arabidops |
| | 28 | 7 | 35.0 | 13 | 9 | AJ593693 | AJ593693 | Arabidops |
| | 29 | 7 | 35.0 | 13 | 9 | AJ593750 | AJ593750 | Arabidops |
| | 30 | 7 | 35.0 | 13 | 9 | AJ594409 | AJ594409 | Arabidops |
| c | 31 | 7 | 35.0 | 13 | 9 | AJ594448 | AJ594448 | Arabidops |
| | 32 | 7 | 35.0 | 13 | 9 | AJ599821 | AJ599821 | Arabidops |
| | 33 | 7 | 35.0 | 14 | 5 | BQ593808 | BQ593808 | E012763-0 |
| | 34 | 7 | 35.0 | 14 | 9 | AJ587585 | AJ587585 | Arabidops |
| | 35 | 7 | 35.0 | 14 | 9 | AJ592722 | AJ592722 | Arabidops |
| | 36 | 7 | 35.0 | 14 | 9 | AJ592942 | AJ592942 | Arabidops |
| | 37 | 7 | 35.0 | 15 | 7 | CF304766 | CF304766 | ABF1--05- |
| | 38 | 7 | 35.0 | 15 | 9 | AJ593961 | AJ593961 | Arabidops |
| | 39 | 7 | 35.0 | 15 | 9 | AJ595331 | AJ595331 | Arabidops |
| | 40 | 7 | 35.0 | 16 | 4 | BG926060 | BG926060 | HNC23-1-E |
| | 41 | 7 | 35.0 | 16 | 5 | BQ588621 | BQ588621 | E012562-0 |
| | 42 | 7 | 35.0 | 16 | 7 | CF323664 | CF323664 | HDN--04-H |
| c | 43 | 7 | 35.0 | 16 | 9 | CL437728 | CL437728 | PST6187-N |
| | 44 | 7 | 35.0 | 17 | 9 | AJ587904 | AJ587904 | Arabidops |
| | 45 | 7 | 35.0 | 18 | 4 | BG927414 | BG927414 | HNC1-1-H3 |